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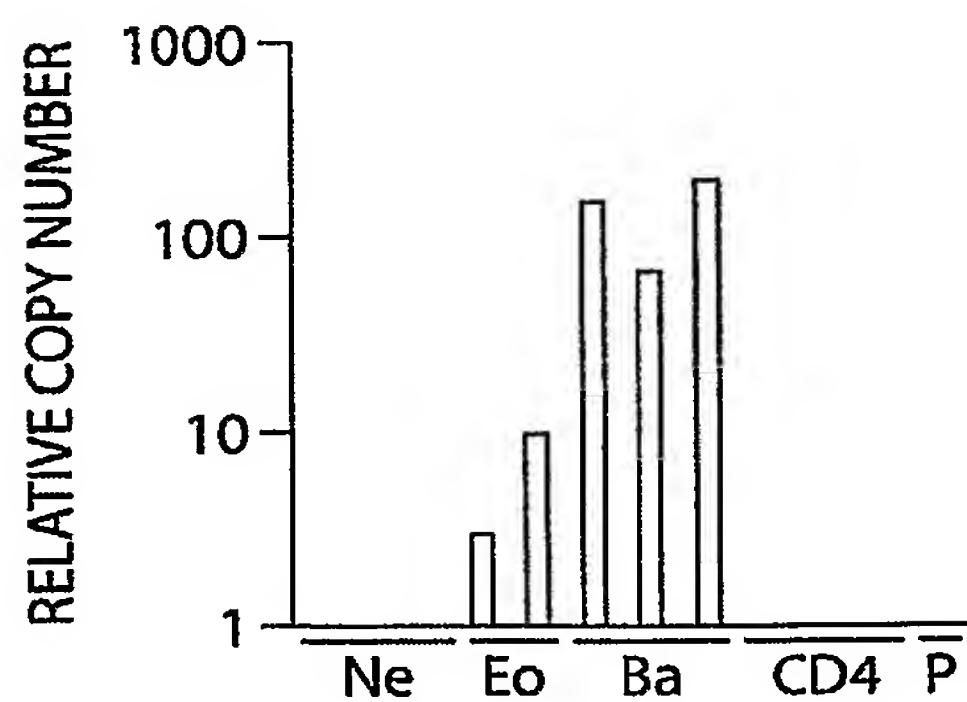


Fig. 1A

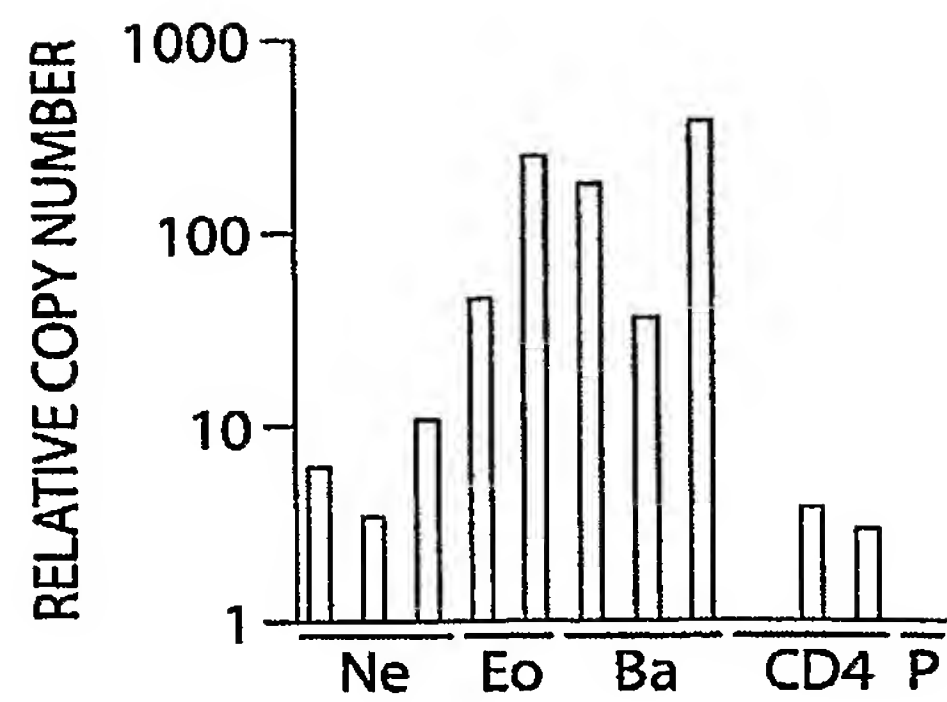


Fig. 1B

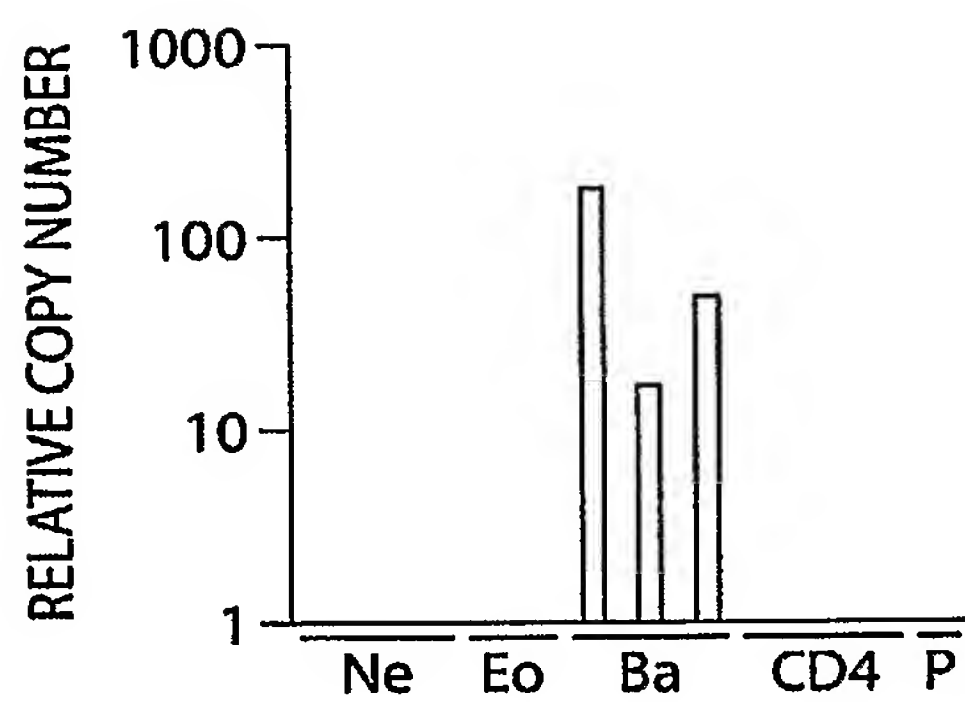


Fig. 1C

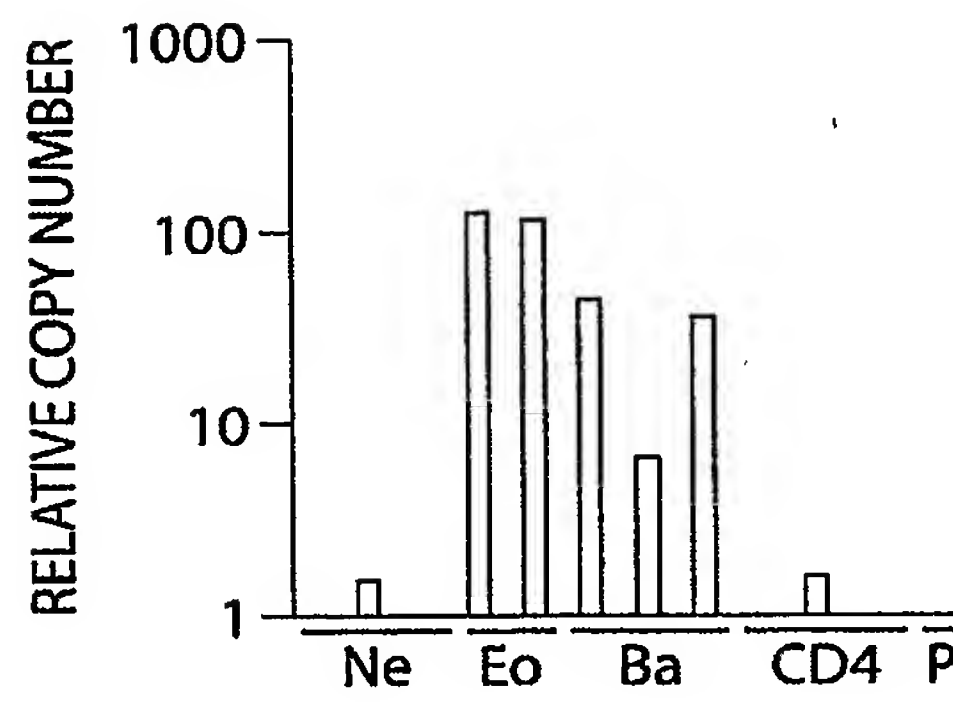


Fig. 1D

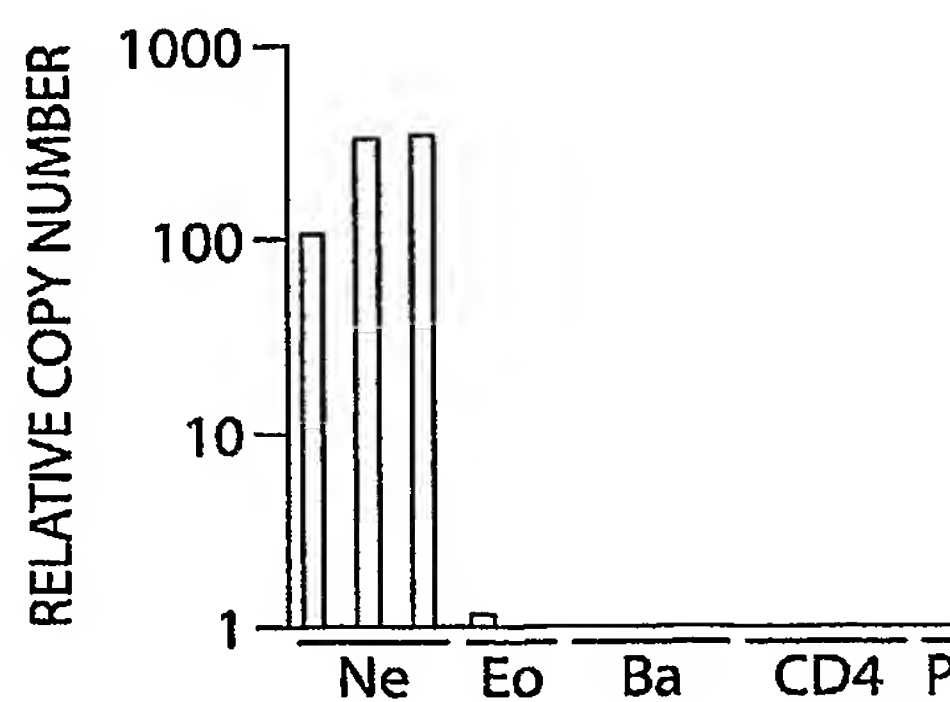


Fig. 1E

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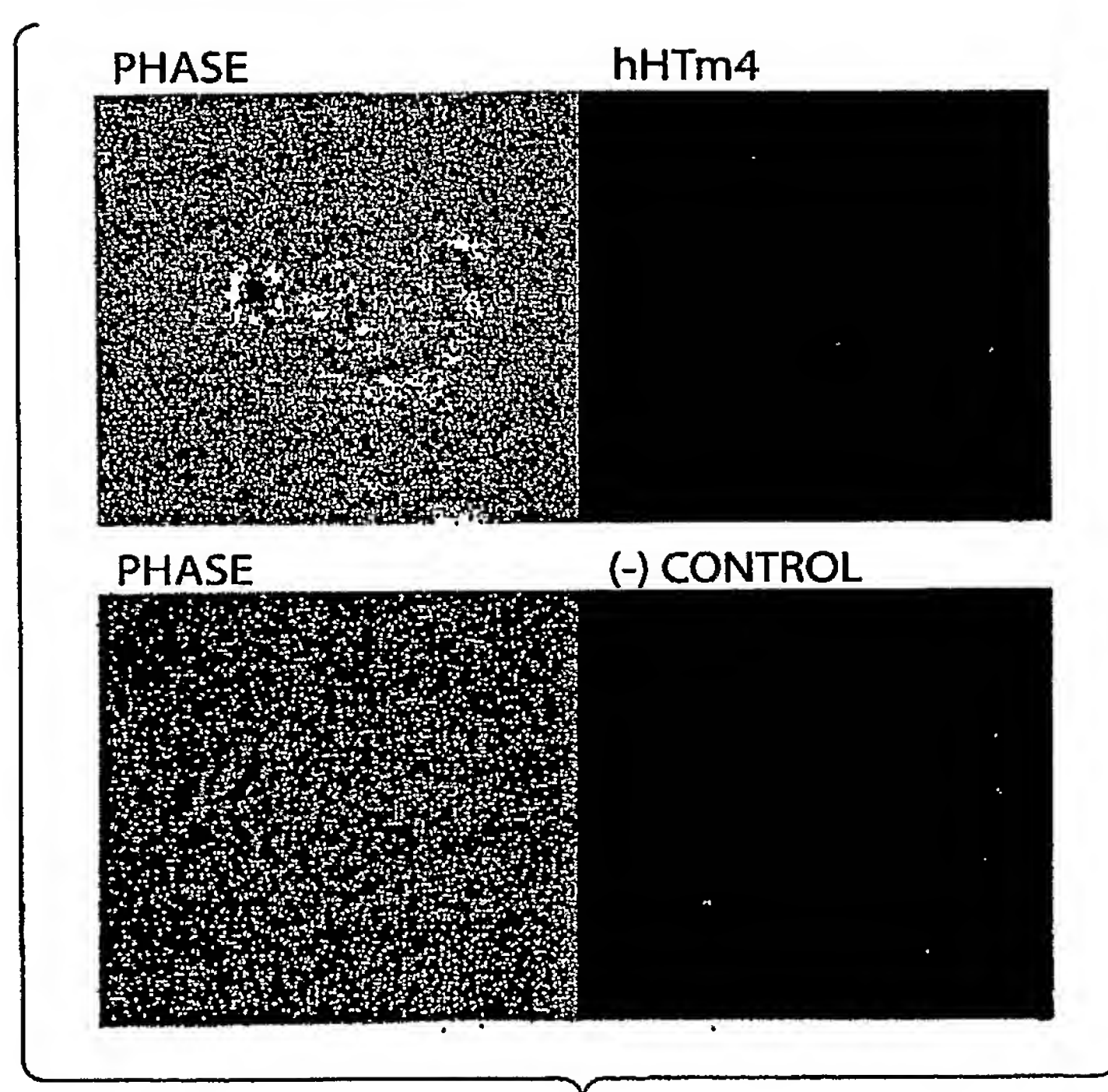


Fig. 2

Figure 3. Granulocyte subtype-specific transcripts for ion channels and receptors

<u>Ion Channels</u> Transcript (Accession #, GenBank)	Cell- type ^a	MC	Ba	Eo	Ne	Pl	CD4	CD8	CD14	CD19	Fb	TC ^b	Gene Functions
<u>Ca²⁺ channel type A1 D</u> (BE550599) <u>aquaporin 9</u> (NM_020980) 602914	Ba, Eo Ne	0.1 0.7	1.7 0.1	1.5 0.4	0.4 137.4	0.0 0.4	0.3 0.9	0.1 0.1	0.0 8.6	0.3 0.1	0.0 0.2	0 7	facilitates uptake of the metalloids arsenite and antimonite
K ⁺ channel Kir 1.3 (U73191) 600359	Ne	0.9	0.2	0.4	99.5	0.7	0.2	0.0	0.8	0.0	0.0	5	Andersen syndrome (170390) and Bartter syndrome (241200)
K ⁺ channel Kir 2.1 (AF153820) 600681	Ne	0.7	3.8	5.3	40.7	0.4	0.2	0.5	1.5	0.7	1.1	6	Andersen syndrome (170390) and Bartter syndrome (241200)
<u>GPCR</u> <u>histamine H₄ R</u> (AF312230) 606792	Ba	0.7	34.2	9.4	0.7	0.4	0.8	0.5	0.6	0.0	0.1	0	expression of HRH4 conferred sensitivity
<u>PGE⁺ R type 3a2</u> (X83858) 176806 <u>C3a R</u> (U62027) 605246 <u>CCR3</u> (NM_001837) 601268	Ba Ba, Eo Ba, Eo	0.8 11.8 0.6	10.3 55.7 117.4	0.1 39.4 90.9	0.7 2.0 24.9	0.6 1.6 0.2	0.3 1.6 0.5	0.2 1.5 0.4	0.2 3.0 0.2	0.5 0.6 0.2	1.7 0.5 0.4	0 3 0	signaling pathways anaphylatoxin receptor importance for eosinophil responses
CRTH2 (NM_004778) 604837	Ba, Eo	1.1	26.0	38.2	2.0	0.8	1.4	1.0	1.2	0.9	0.5	0	mediate signals to the interior of the cell via activation of heterotrimeric G proteins
<u>EMR-1</u> (NM_001974) 600493	Ba, Eo	0.8	33.5	90.9	4.2	3.4	1.7	0.8	7.1	1.6	0.5	1	Probably involved in cellular response to a hormone
adenosine A ₃ R (NM_000677) 600445 P2Y2 purinergic R (NM_002564) 600041	Eo Eo	2.6 0.1	2.9 0.1	15.4 5.5	2.3 0.1	1.2 0.2	1.6 0.1	0.5 0.3	2.0 1.2	0.5 0.2	0.5 0.1	0 0	cardioprotective function P2RY2 may participate in control of the cell cycle of endometrial carcinoma cells
GPR 105 purinergic R (NM_014879)	Eo	2.6	2.9	15.4	2.3	1.2	1.6	0.5	2.0	0.5	0.5	2	GPR105 is a G-protein-coupled receptor identifying a quiescent, primitive population of hematopoietic cells restricted to bone marrow; GPR105 might play an important role in peripheral and neuroimmune function
GPR, Edg-4 (AF011466) 605110	Eo, Ne	1.3	2.8	15.9	24.2	0.1	3.6	5.0	3.8	1.9	0.9	2	edg-4 mrna was expressed in mouse islets; edg-4 (lpa2) r is a distinctive functional marker for ovarian carcinoma, and is expressed both as the wild-type and a carboxyl-terminally extended gain-of-function mutant.
PAR1-like GPR43 (NM_005306)	Eo, Ne	0.3	0.7	12.4	35.2	0.8	0.1	0.1	0.7	0.4	0.1	0	the highest levels of gpr43 were

Fig. 3A

<u>603823</u>														
<u>found in immune cells; gpr43 is highly restricted in hematopoietic tissues</u>														
C5a R (NM_001736)	113995	Ne	2.3	21.6	13.6	92.6	2.3	1.2	0.5	25.6	1.0	0.4	5	receptor for the chemotactic and inflammatory peptide anaphylatoxin c5a. this receptor stimulates chemotaxis, granule enzyme release and superoxide anion production.
CXCR1 IL-8R (NM_000634)	146929	Ne	0.2	4.3	0.3	83.4	0.4	0.3	0.2	0.2	0.1	0.1	0	receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to mgsa (gro) with a low affinity.
CXCR2 IL-8R (NM_001557)		Ne	0.2	1.1	1.5	112.1	2.7	0.3	0.8	0.7	0.6	0.0	1	receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. binding of il-8 to the receptor causes activation of neutrophils. this response is mediated via a g-protein that activate a phosphatidylinositol-calcium second messenger system. this receptor binds to il-8 with a high affinity and to gro/mgsa and nap-2 also with a high affinity.
formyl peptide R 1 (NM_002029)	136537	Ne	2.8	23.5	8.8	282.9	3.6	1.3	0.7	62.6	1.1	0.5	0	HIGH AFFINITY RECEPTOR FOR N-FORMYL-METHIONYL PEPTIDES, WHICH ARE POWERFUL NEUTROPHILS CHEMOTACTIC FACTORS. BINDING OF FMLP TO THE RECEPTOR CAUSES ACTIVATION OF NEUTROPHILS. THIS RESPONSE IS MEDIATED

Fig. 3B

Fig. 3B

Fig. 3C												VIA A G-PROTEIN THAT ACTIVATES PHOSPHATIDYLINOSITOL- CALCIUM SECOND MESSENGER SYSTEM. likely FPR2, mediates superoxide production at high concentrations of fMLF C5L2 is an anaphylatoxin- binding protein with unique ligand binding and signaling properties GPR86 proved to be a G(i)- coupled receptor displaying a high affinity for ADP, similar to the P2Y(12) receptor and can therefore be tentatively called P2Y(13) PAR2 plays a key role in chronic joint inflammation responsible for initiating the allergic response Cell cycle regulator promotes the proliferation and differentiation of hematopoietic cells engagement of 2B4 wih specific antibody activates NK cytolytic activity Receptor for acidic and basic fibroblast growth factors. lacking either 115ra or Sox4 have defects in B-cell development SIGLEC8 expression on eosinophils but not other leukocytes Signaling from the KIT receptor tyrosine kinase is essential for primordial germ cell growth both in vivo and in vitro OBBP1 is almost exclusively expressed on B cells. MS4A2 Allergic disease receptor-mediated endocytosis
formyl peptide R 2 (<u>U81501</u>)	Ne	0.4	0.5	0.6	75.5	0.1	1.0	0.6	6.0	0.8	0.1	5
GPR77 (<u>NM_018485</u>)	Ne	0.1	0.9	0.8	3.4	0.0	0.3	0.2	1.0	0.1	0.3	2
GPR86 purinergic R (<u>NM_023914</u>)	Ne	0.3	0.2	17.9	88.2	1.9	0.1	0.2	12.3	0.6	0.0	1
PAR2 (<u>BE965369</u>) <u>600933</u>	Ne	0.1	0.3	2.2	36.2	0.1	0.7	0.1	1.6	0.4	1.2	15
<u>Other Receptors</u> Fc ε RI α (<u>BC005912</u>) <u>147138</u>	Ba	19.4	219.0	4.6	5.5	1.4	5.1	0.8	1.4	0.4	0.2	0
<u>HTm4</u> (<u>L35848</u>) <u>606498</u>	Ba	0.6	133.1	6.9	3.5	0.2	0.5	0.4	0.1	0.2	0.0	1
IL-3 R (<u>NM_002183</u>) <u>308385</u>	Ba	0.6	52.6	2.0	0.7	0.2	0.3	0.2	0.7	0.1	0.1	0
CD244 NK cell R <u>NM_016382</u> <u>605554</u>	Ba, Eo	0.3	56.0	16.5	1.2	0.1	0.4	3.5	5.2	1.1	0.1	0
fibroblast growth factor R 2 (<u>NM_022969</u>) <u>176943</u> IL-5R α (<u>M75914</u>) <u>147851</u>	Ba, Eo	0.1	27.9	12.1	0.2	0.1	0.1	0.2	0.1	0.1	1.0	17
Siglec 8 (<u>NM_014442</u>) <u>605639</u>	Ba, Eo	0.9	20.5	30.4	0.6	0.1	0.1	0.1	0.1	0.2	0.1	0
CD117 c-KIT (<u>NM_000222</u>) <u>164920</u>	Eo	1.8	0.3	17.4	0.4	0.3	0.2	0.1	0.2	0.5	0.2	0
SigtecB D86358 604405	MC	89.0	7.2	4.2	1.2	0.8	0.2	0.5	0.1	0.1	0.5	15
Fc ε RIβ (<u>NM_000139</u>) <u>147138</u> low density lipoprotein R	MC	5.6	0.2	0.0	0.2	0.5	0.0	0.0	0.0	0.4	0.0	0
	MC, Ba	22.3	44.3	0.4	0.6	1.6	0.5	0.2	0.0	0.3	0.1	0
	MC, Ba	20.7	20.4	1.3	1.8	2.3	2.1	3.4	3.5	0.8	6.3	34

<u>(NM_000527) 606945</u> <u>TRK neurotrophin R (NM_002529)</u> <u>191315</u>	MC, Ba	4.6	7.3	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0	participates in the primary signal transduction mechanism of NGF; is also an immunoregulatory cytokine acting on monocytes his gene is mainly expressed in small intestine, colon, testis, and leukocytes
<u>butyrophilin like R (AK025267).</u>	Ne	1.1	1.7	1.5	6.9	1.5	1.7	1.6	0.9	1.5	1.3	1	1	<u>Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha.</u>
<u>CD120a, TNF-R-1 (NM_001065)</u> <u>191190</u>	Ne	1.7	1.2	7.8	74.7	1.3	2.2	5.9	17.4	0.6	16	35	35	<u>The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Contributes to the induction of noncytotoxic TNF effects including anti-viral state and activation of the acid sphingomyelinase.</u>
<u>CD95, Fas, APO-1 (AA164751) 134637</u>	Ne	1.4	10.9	7.3	50.4	1.3	5.6	4.8	3.6	2.6	9.7	7	7	<u>Receptor for TNFSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted</u>

Fig. 3D

isoforms 2 to 6 block apoptosis
(in vitro).
does not induce apoptosis.

failure of the patient's
neutrophils to express Fc
receptor III was associated with
SLE

inhibits cell proliferation and
survival in response to CSF3
promotes the proliferation and
differentiation of hematopoietic
cells

type II receptor inhibits IL1
activity by acting as a decoy
target for IL1

IGFs may elicit a myogenic
event which may be a key
mechanism in the etiology of
breast and ovarian cancer
Mutation in either MPRD or
MPRI might result in a clinical
disorder resembling a
mucoepidermoid

Eosinophils may be activated
through L1R7 for release of
eosinophil-derived neurotoxin
that TLR2-TLR1 heterodimers
mediated the strongest cell
activation

TLR2 is a molecular link
between microbial products,
apoptosis, and host defense
mechanisms
immunostimulatory activity

decoy R1, TRAILR3 (AF012536) 603613	Ne	0.1	1.5	7.7	78.7	0.5	0.2	0.1	0.7	0.1	0.6	0
FCyR IIc2 (U90939)	Ne	1.5	2.4	7.8	59.9	0.3	0.2	0.1	7.2	2.3	0.2	2
FCyR IIc3 (U90940)	Ne	2.4	10.7	10.0	84.3	3.0	1.4	0.6	14.0	7.2	1.0	5
FCyR III (J04162) 146740	Ne	0.7	1.6	1.9	199.6	6.6	1.3	1.3	2.2	2.6	0.1	4
G-CSF R (NM_0007601) 138971	Ne	0.1	0.4	1.6	163.6	0.2	0.8	0.2	25.5	0.1	0.2	3
IL-13 R (U81379) 308385	Ne	0.3	0.2	2.0	14.1	0.4	0.4	0.3	2.9	1.3	1.3	0
IL-1R, type II (NM_004633) 147811	Ne	0.1	0.1	0.1	53.5	0.2	0.4	0.1	0.2	0.0	0.0	3
IGFR 1 (NM_000875) 147370	Ne	0.3	3.5	5.0	17.4	1.6	0.1	2.8	2.4	2.0	3.5	3
IGFR 2 (NM_000876) 147280	Ne	4.6	0.9	5.4	85.3	1.7	2.9	8.7	8.4	4.8	15	32
leukocyte immunoglobulin-like R A2 (NM_006866) 604812	Ne	0.5	5.8	4.3	41.2	1.8	0.0	0.1	11.6	0.5	0.1	2
Toll-like R 1 (AL050262) 601194	Ne	0.6	0.3	1.2	31.5	1.6	0.8	0.7	3.0	1.5	0.3	0
Toll-like R 2 (NM_003264) 603028	Ne	0.9	6.0	1.3	83.8	1.6	1.3	0.1	26.3	0.9	0.4	0
Toll-like R 6 (NM_006068)	Ne	0.5	1.0	0.9	8.8	0.1	0.9	0.9	2.1	1.2	0.6	0

a. Cell-type specificity was obtained by comparing the "normalized AD" levels of each gene in mast cells (MC; average of 2 experiments), basophils (Ba; average of 3 experiments), eosinophils (Eo; average of 4 experiments), neutrophils (Ne; average of 4 experiments), platelets (Pl), CD4⁺ cells (CD4), CD8⁺ cells (CD8), CD14⁺ cells (CD14), CD19⁺ cells (CD19) and nasal polyp-derived cultured fibroblasts (Fb).

Fig. 3E

	CB cultured		Basophils	cultured basophils	Eosinophils		Neutrophils		platelets	Erythrocytes	CD4	CD8	CD14	CD19
	MCs													
Spink5	21		17	11	22	16	30	15	28	36	129	104		
chymase human	1221		47	65	45	12	101	62	108	59	104	45		
tryptase alpha	21179		212	40	33	25	184	139	104	17	52	39		
tryptase beta	25414		195	113	49	28	152	10	122	113	93	6		
tryptase delta	349		45	6	23	55	74	113	11	10	42	11		
tryptase gamma	654		56	19	38	78	28	24	81	230	142	83		
TRPV2	129		37	15	97	99	259	137	133	67	97	110		
ANKTM1_	28		28	8	38	30	96	18	14	46	11	28		
Cannabinoid receptor type 1	50		41	14	47	36	27	61	41	56	18	54		
Cannabinoid receptor type 2	160		369	226	578	177	271	530	324	232	212	421		

Fig. 4A

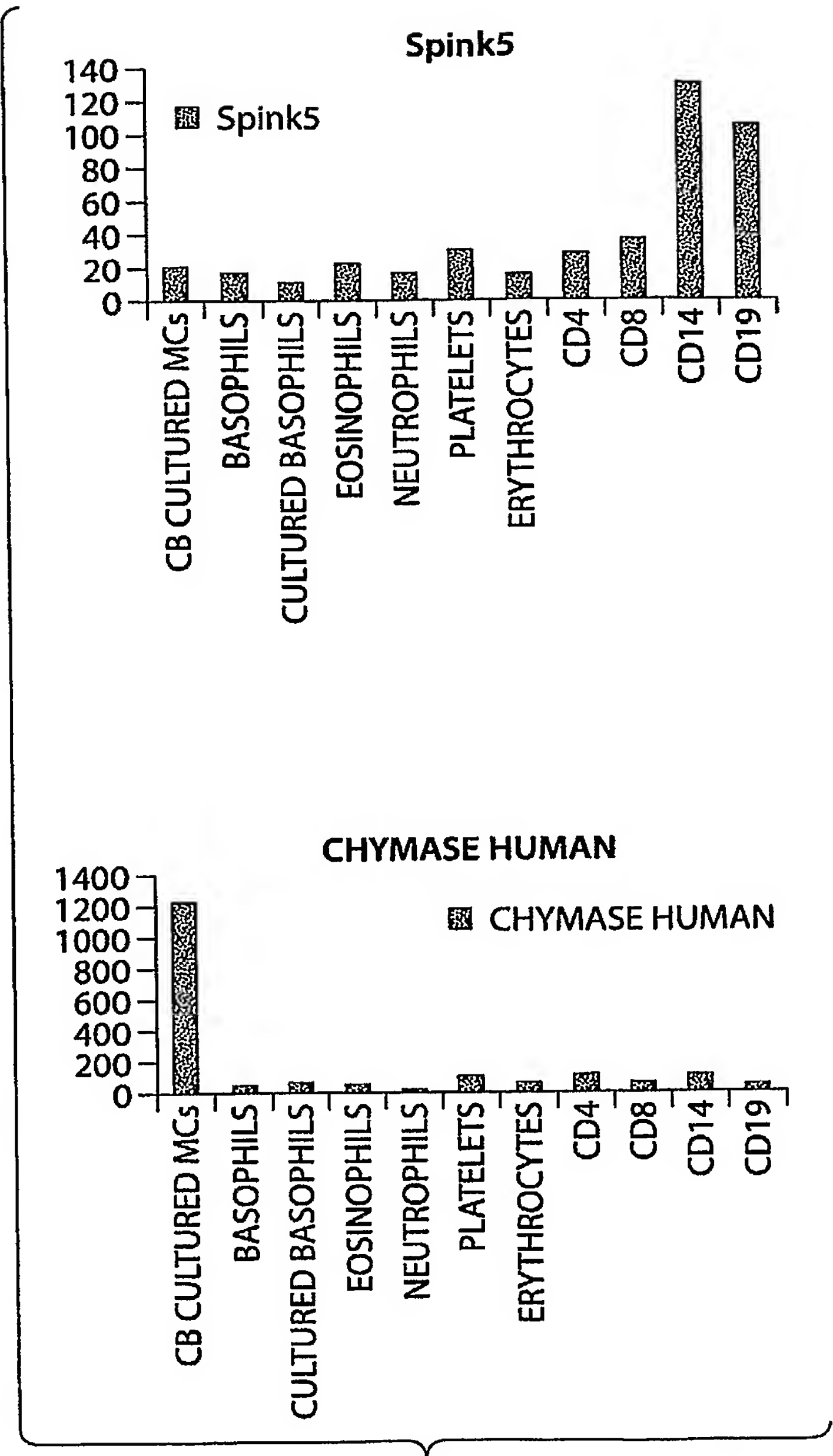


Fig. 4B

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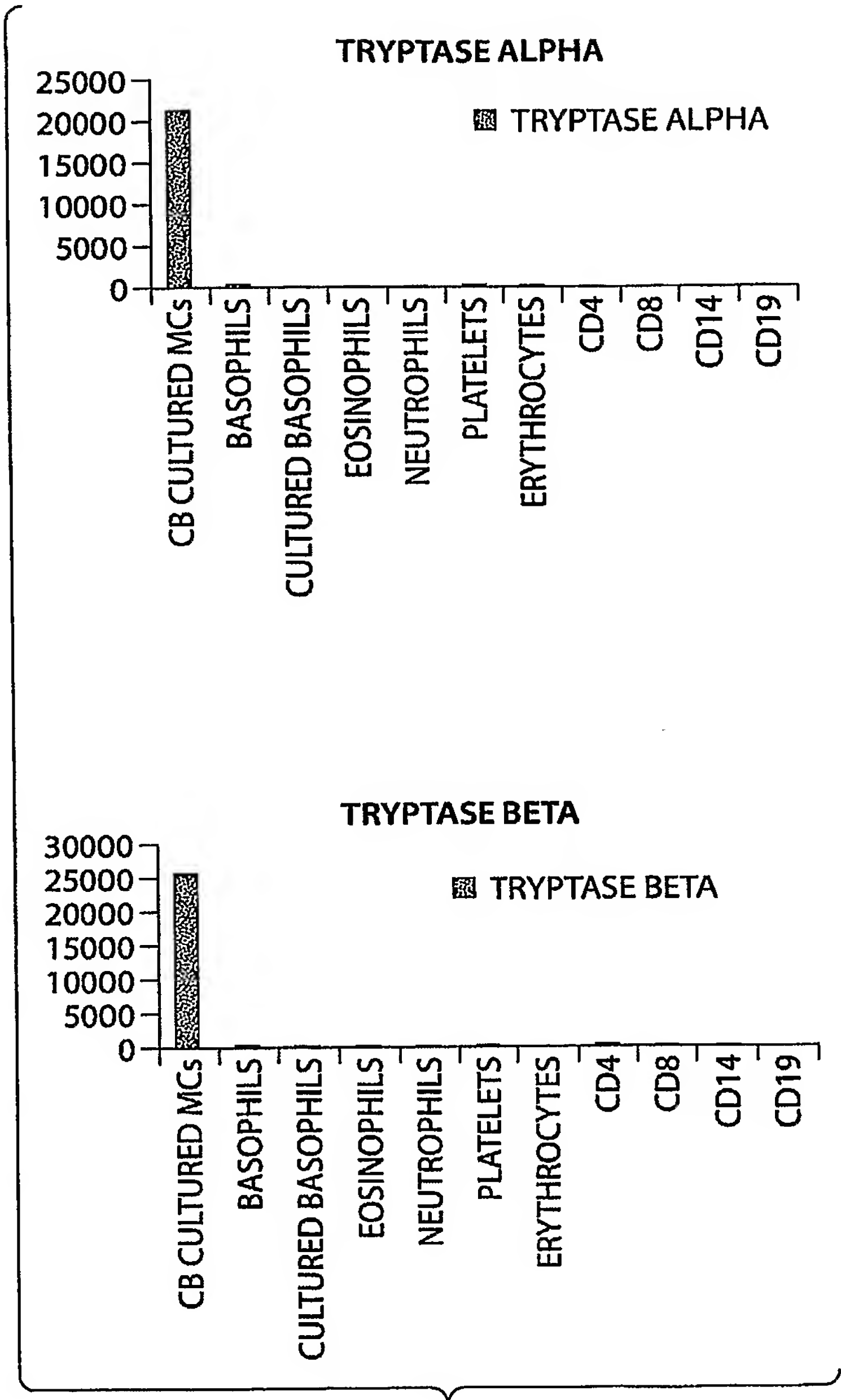


Fig. 4C

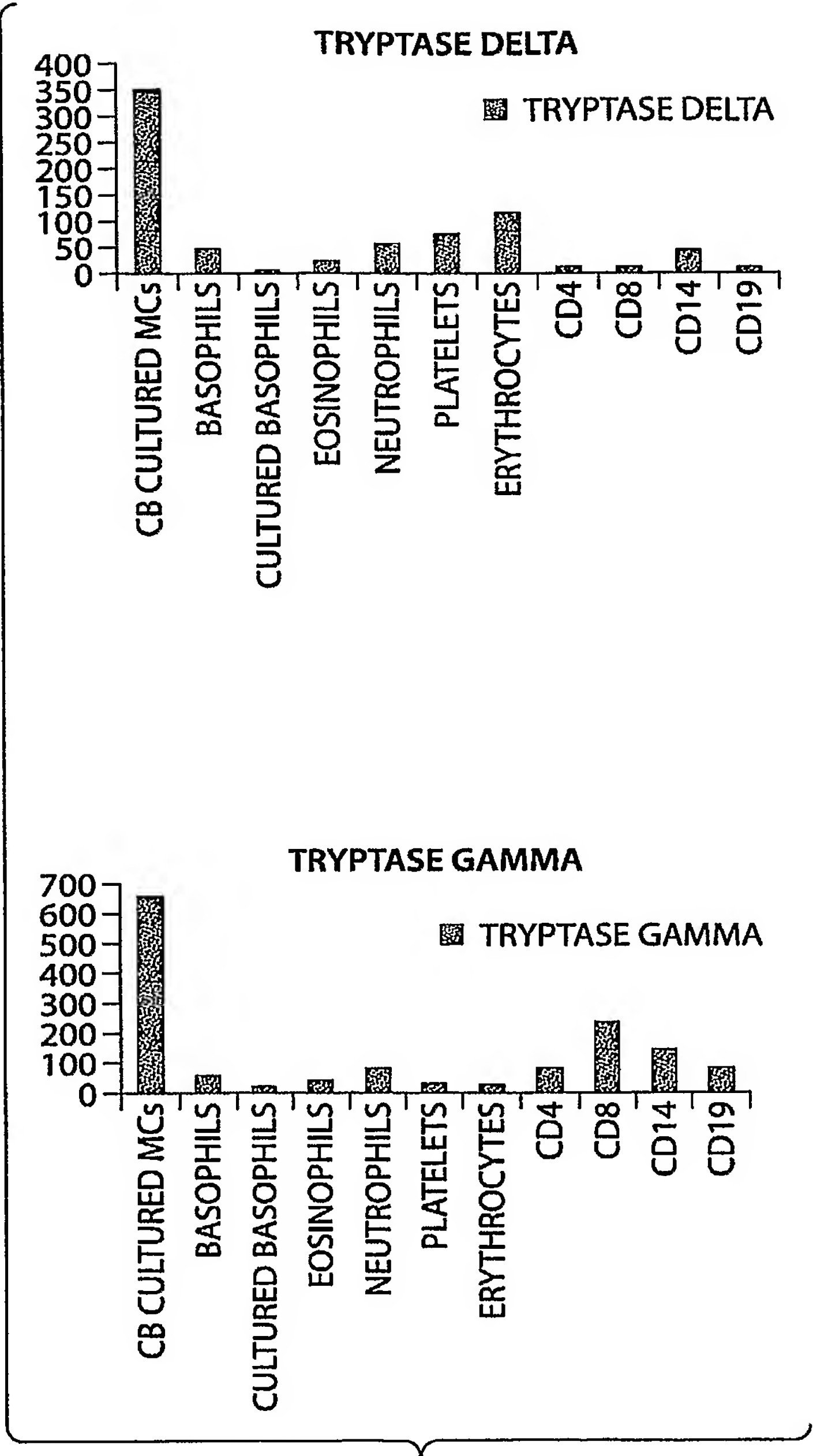


Fig. 4D

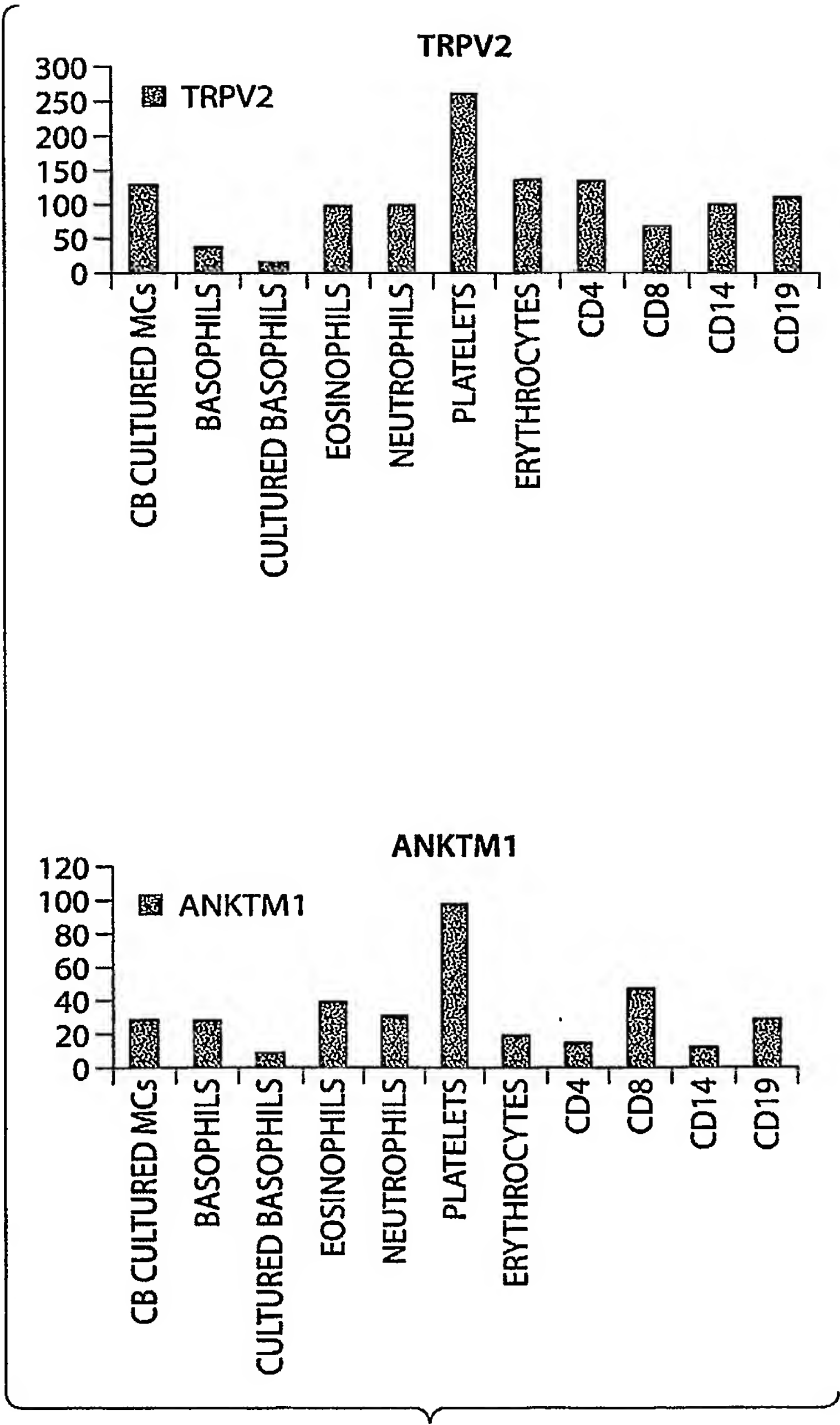


Fig. 4E

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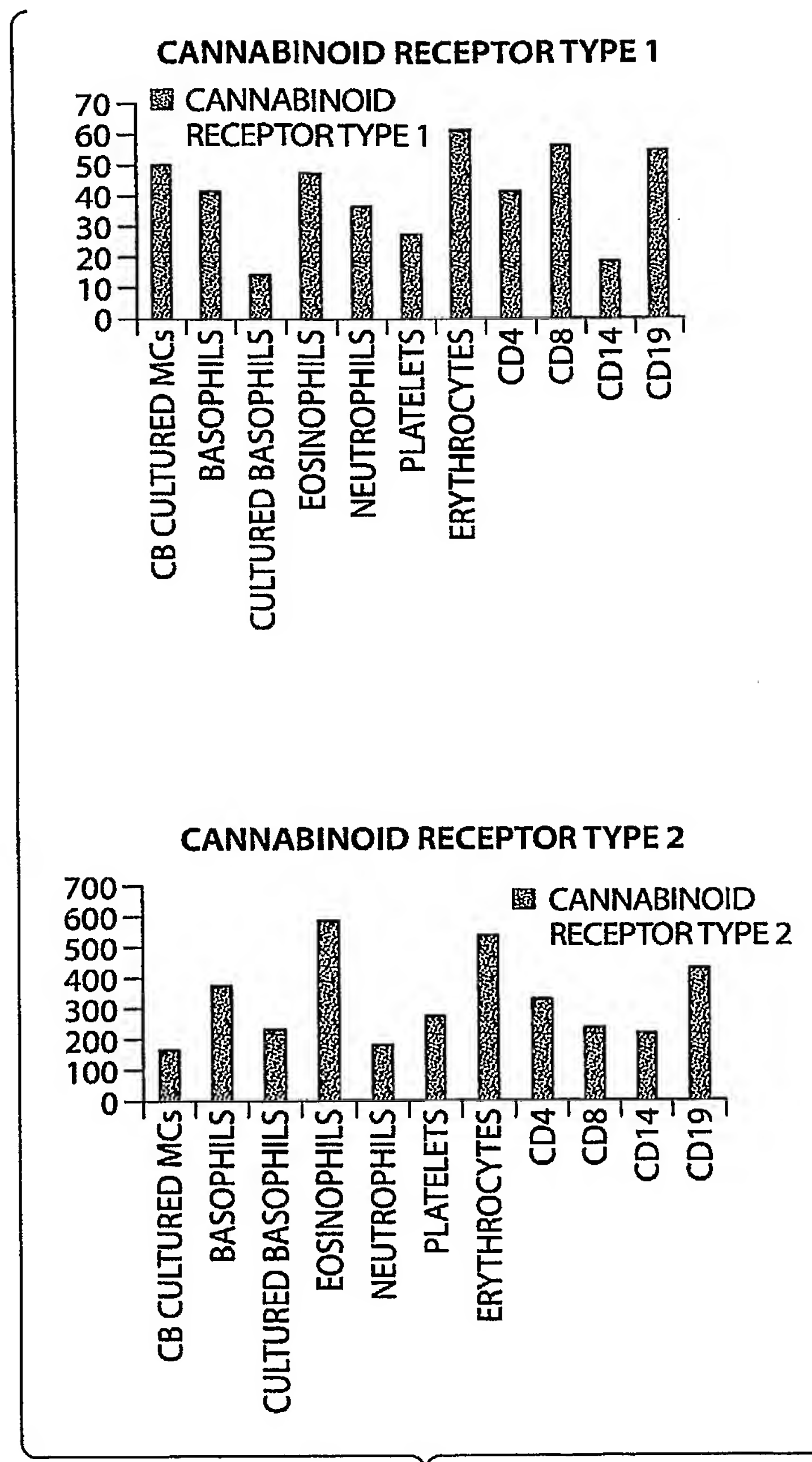


Fig. 4F

CB cultured MCs		Basophils	cultured basophils	Eosinophils	Neutrophils	platelets	Erythrocytes	CD4	CD8	CD14	CD19
KIR2BS	86	28	39	26	37	125	46	103	95	85	28
KIR2B3	4	45	1004	59	84	18	68	31	68	451	13
KIR2B1	165	84	51	258	1261	31	42	13	18	1105	125
KIR2B2	375	780	227	1755	4237	199	375	286	58	2963	214
KIR2A2	49	614	384	461	3269	146	318	8	9	1247	52
KIR2A1	28	50	45	154	389	120	148	127	35	539	86
KIR3DL2	7	58	34	18	23	13	106	14	286	68	204
KIR2BS3	22	17	21	27	28	35	11	28	110	88	111
KIR2DL3 VARIANT	30	54	134	66	61	149	95	39	247	147	271
KIR2DS1	35	138	81	88	93	191	132	57	257	21	267
KIR2DS5	24	31	23	21	21	53	27	33	135	19	173
KIR2DL4	139	140	85	157	144	280	210	35	239	152	196
KIR2DL4	11	45	41	50	41	88	15	19	72	77	85
KIR5123FM	41	43	31	20	52	31	121	96	163	26	193
KIR2DL53	27	83	24	41	49	61	239	92	323	56	72
KIR3DL1	68	89	41	51	95	75	97	76	169	36	196
MIR cl-10	144	621	83	1334	2386	107	146	145	52	2154	99
PTPRF	18	14	5	28	37	86	12	13	14	32	23

Fig. 5A

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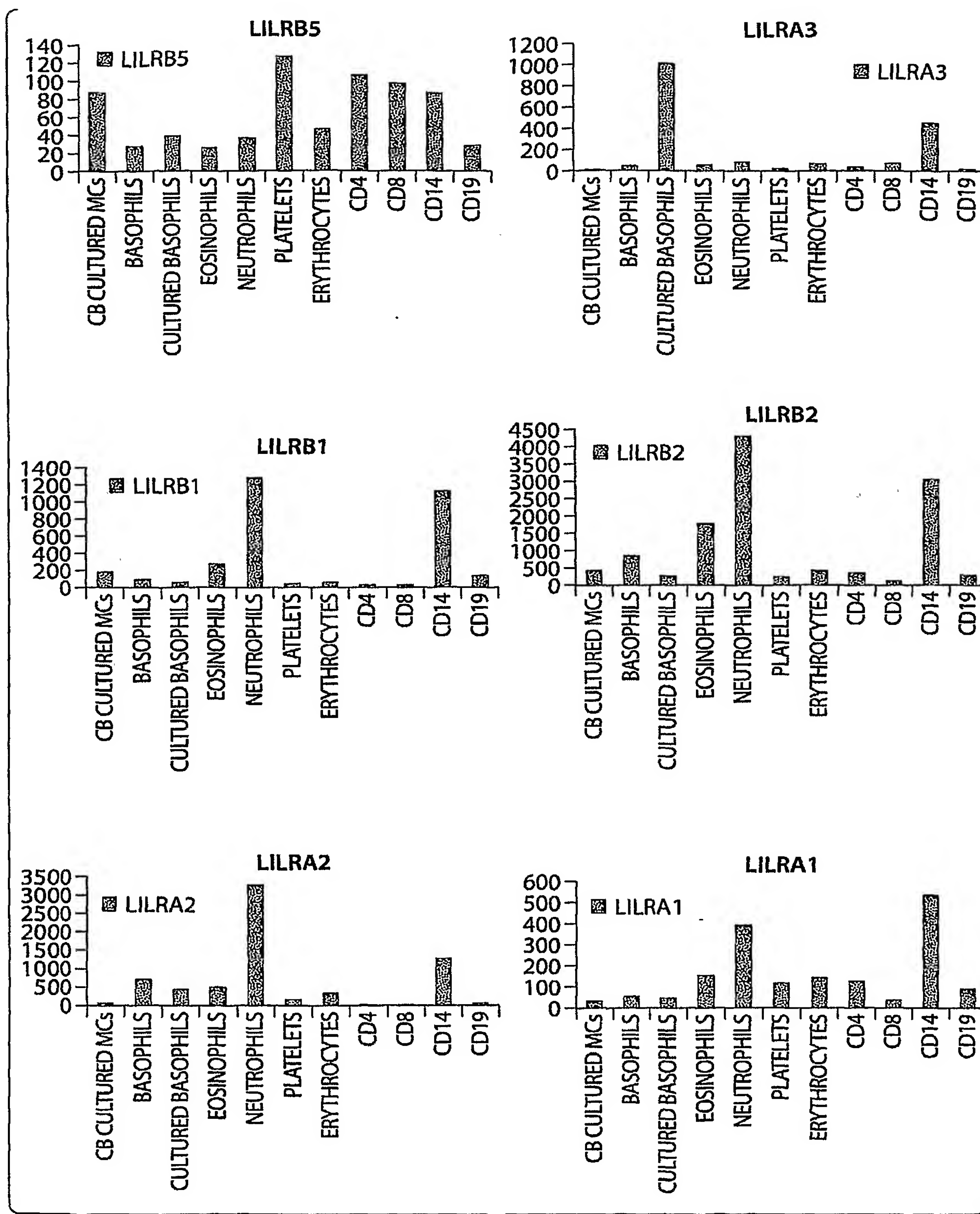


Fig. 5B

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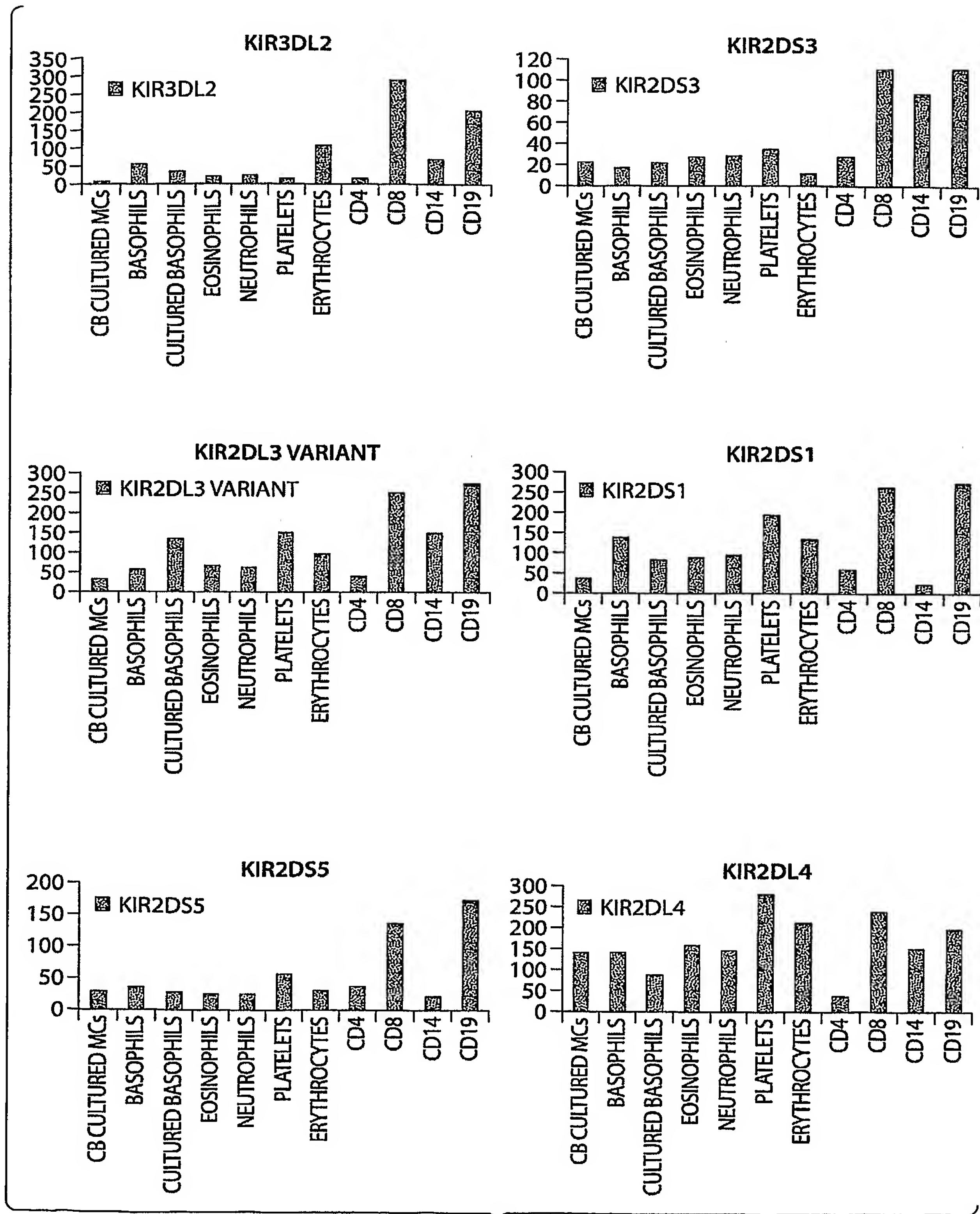


Fig. 5C

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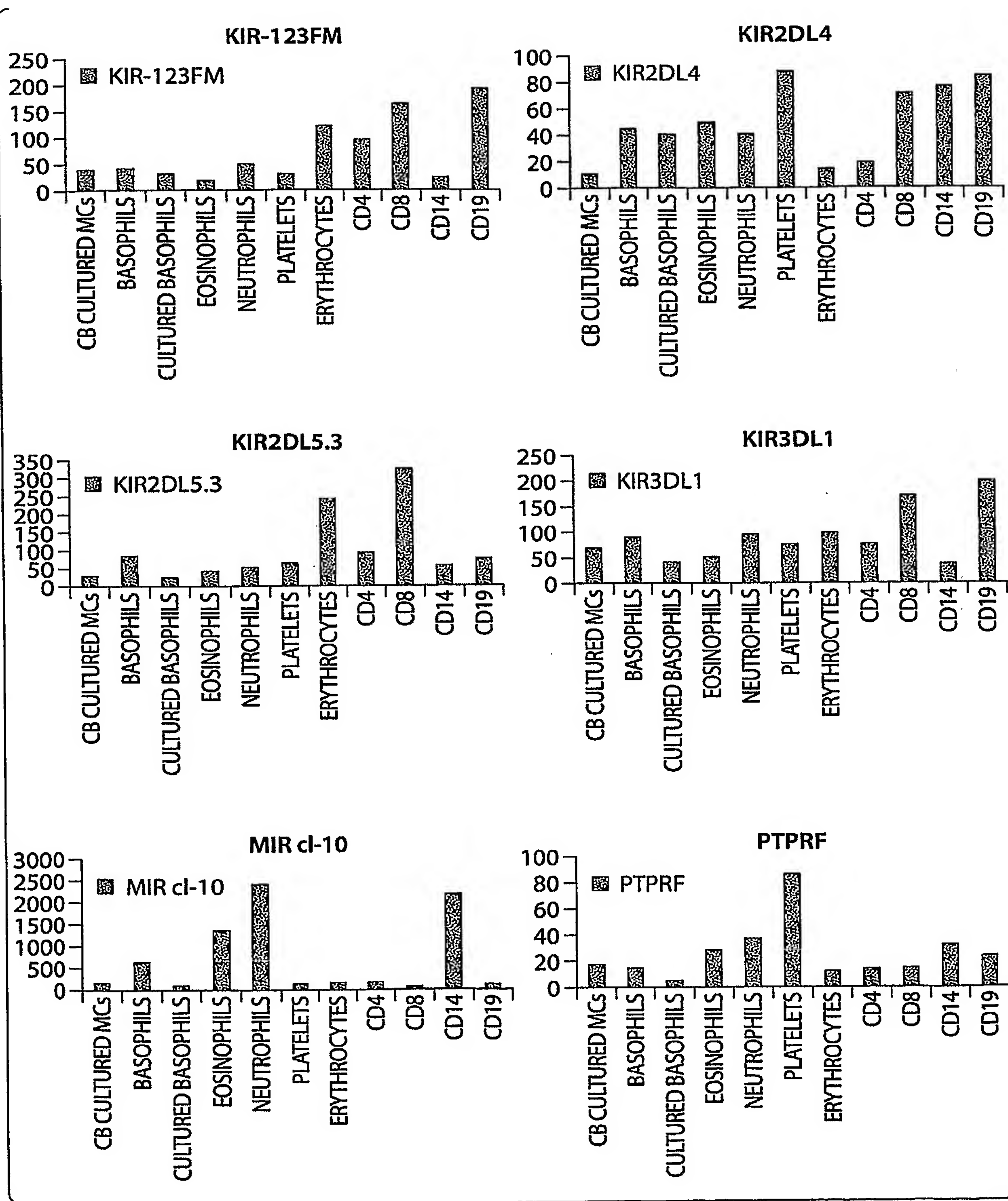


Fig. 5D

Table E1. The complete list of granulocyte subtype-selective transcripts. Selectivity index (S.I.) was calculated by comparing the "normalized AD" level of a cell type or of two cell types with the maximal gene expression level of the other 8 or 9 cell types including platelets (Pl), CD4⁺ cells, CD8⁺ cells, CD14⁺ cells, CD19⁺ cells and nasal polyp-derived cultured fibroblasts (Fb). When the result was accompanied by presence call, it was shown as a bold numeral. Italic numerals show that the raw AD levels were associated with absence call by the GeneChip analysis software. Transcripts having S.I. >3-fold were shown in A-H. Abbreviations used in the table through A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

A. Basophil (Ba)-selective transcripts (1/2).

Probe set	Accession #	Transcripts	MC		Ba 1	Ba 2	Ba 3		Eo 1	Eo 2	Eo 3		Eo 4	Ne 1	Ne 2	Ne 3		Ne 4	pl	CD4	CD8	CD14	CD19	Fb	Ba S.I.
			cord	lung	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)	(small)
207539_s_at	NM_000589.1	IL-4	0.2	0.1	10.4	16.9	13.4	0.1	0.0	0.2	0.1	0.1	0.3	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.1	0.0	0.0	0.0	73.348
210254_at	L35848.1	HTm4	0.8	0.4	115.6	130.1	153.6	2.4	1.7	21.8	1.7	0.1	0.9	3.6	9.5	0.2	0.0	0.0	0.0	0.5	0.4	0.1	0.2	0.0	38.24
205513_at	NM_001062.1	vitamin B12 binding protein	1.5	1.2	98.9	149.3	110.9	3.2	2.2	16.1	1.9	4.9	4.5	6.3	8.1	1.8	0.1	0.1	0.1	0.7	0.8	1.4	0.9	0.1	20.322
206148_at	NM_002183.1	IL-3R	1.0	0.1	6.2	80.2	71.3	1.7	1.7	1.8	2.9	0.3	0.4	0.2	1.9	0.2	0.1	0.1	0.1	0.2	0.2	0.7	0.1	0.1	16.62
214920_at	R33964	FLJ11022 fis	0.1	1.1	4.9	13.1	15.4	0.1	0.2	0.7	0.5	1.0	0.4	0.5	0.7	0.1	0.1	0.1	0.1	0.2	0.1	0.3	0.3	0.1	16.049
201825_s_at	AL572542	CGI-49	3.3	1.6	21.4	74.9	46.5	2.1	1.2	0.1	1.2	0.1	0.1	0.2	0.1	1.3	0.7	1.7	0.9	1.7	1.4	0.8	2.8	0.1	15.045
213238_at	AI478147	ATPase, Class V, type 10D	1.2	2.9	39.9	76.3	118.9	2.3	1.7	3.1	1.9	2.1	1.4	2.3	6.8	0.7	0.9	0.9	0.9	0.9	2.5	5.0	4.1	0.2	14.398
211734_s_at	BC005912.1	Fc epsilon R1 alpha	10.5	28.4	210.0	220.8	226.2	8.4	2.1	4.8	2.9	0.3	0.7	4.5	16.6	1.4	5.1	0.8	0.1	0.8	1.4	0.4	0.2	0.2	12.703
213894_at	BF447246	KIAA0960	0.1	0.0	3.7	13.0	15.6	0.3	0.4	0.4	0.4	0.9	0.7	0.7	0.6	0.5	0.6	0.1	0.6	0.7	0.1	0.2	0.2	0.2	12.272
206363_at	NM_005360.2	G-MAF	3.7	1.4	36.5	75.7	66.4	1.2	0.1	0.2	0.2	0.2	0.1	0.2	1.0	0.6	4.8	2.7	3.5	2.7	0.5	1.0	0.0	0.0	11.927
203373_at	NM_003877.1	SOC2	2.1	3.9	21.7	85.0	112.2	4.6	4.7	9.4	6.5	0.7	1.2	0.3	2.5	1.6	3.2	3.5	0.8	0.3	0.1	0.9	3.6	0.1	9.8282
207538_at	NM_000589.1	IL-4	0.3	0.1	5.4	9.8	9.2	0.4	0.4	0.0	0.3	0.1	0.0	0.4	0.7	0.8	0.4	0.3	0.1	0.3	0.1	0.0	0.1	0.1	9.8156
213694_s_at	BF671400	LIM-protein	0.6	0.1	11.1	21.0	20.6	1.9	1.6	2.4	1.8	0.8	0.6	1.5	2.5	0.1	0.0	0.3	1.0	0.3	1.0	0.0	0.1	0.1	8.9245
209360_s_at	D43968.1	AML1b protein	10.4	2.4	53.2	131.1	90.5	8.5	7.0	13.8	11.3	0.5	0.5	0.5	4.2	1.3	4.1	5.9	1.3	4.1	1.3	2.5	3.1	0.1	8.7543
220234_at	NM_004056.2	carbonic anhydrase VIII	0.4	0.1	11.7	10.2	6.0	1.2	0.1	0.2	0.4	0.8	0.9	0.1	0.5	0.5	1.1	0.1	1.1	0.1	0.1	0.1	0.8	0.0	8.1309
210643_at	AF053712.1	osteoprotegerin ligand	0.1	0.3	1.8	3.4	6.0	0.7	0.4	0.3	0.2	0.4	0.1	0.3	0.1	0.1	0.3	0.4	0.3	0.4	0.3	0.2	0.2	0.2	7.6628
209211_at	AF132818.1	colon Kruppel-like factor	0.1	0.0	1.8	10.2	8.8	0.3	0.5	1.5	0.8	1.1	0.7	0.8	0.5	0.2	0.2	0.4	0.2	0.4	0.2	0.1	0.3	0.3	7.239
204309_at	NM_000781.1	CYP11A	0.3	0.1	2.6	6.1	5.6	0.1	0.3	0.5	0.5	1.0	0.1	0.1	0.9	0.3	0.3	0.1	0.3	0.1	0.0	0.3	0.7	0.7	6.8366
203372_s_at	AB004903.1	SOC2	0.6	1.6	9.2	8.5	15.9	1.4	2.4	0.9	0.2	0.7	0.6	0.4	0.8	0.8	1.6	1.3	1.6	1.3	0.3	0.3	1.4	0.1	6.8271
207463_x_at	NM_002771.1	serine protease 3 (trypsin 3) acid sphingomyelinase-like	1.0	1.0	4.8	10.0	10.9	0.4	1.0	1.0	1.2	1.2	0.9	1.0	1.8	0.4	0.6	0.4	0.6	0.6	0.4	0.3	0.7	1.2	6.7218

Fig. 6A-1

Fig. 6A-2

A. Basophil (Ba)-selective transcripts (2/2).

MC	cord blood	Transcripts	Accession #	Probe set	20/36																					
					MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	BaSL			
0.6	0.6	class 1 homeoprotein (HOXA9)	U41813.1	214651_s_at	1.7	63	32	83	0.3	0.5	0.8	0.5	0.1	0.1	0.5	1.0	1.0	0.1	0.1	0.3	0.1	0.1	0.3	0.1	0.1	4.3618
1.6	1.9	DKFZp434D0316_s1	AL041124	32502_at	146	225	174	4.0	2.1	0.7	0.7	1.4	1.1	1.0	0.4	0.4	2.3	2.5	4.1	2.5	2.3	1.8	2.3	1.8	4.3594	
0.2	0.1	catenin (cadherin-associated protein) alpha 2	NM_004389.1	205373_at	1.1	3.9	3.2	0.6	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.6	0.2	0.2	0.2	0.2	0.2	4.2308
0.3	0.7	FLJ22191	NM_025231.1	219676_at	2.5	73	120	0.9	0.2	2.0	2.0	1.5	0.2	1.1	4.2	2.2	0.6	1.1	1.4	0.3	1.4	0.1	0.1	0.1	0.1	4.2135
4.7	3.1	beta2-chimaerin	AK026415.1	213385_at	83	229	21.8	1.1	0.8	0.9	0.9	1.0	0.2	1.5	0.8	1.0	0.1	0.9	1.6	3.3	0.2	0.4	0.4	0.4	0.4	4.2131
0.4	0.0	oncostatin M	BG437034	214637_at	0.9	54	4.4	0.2	0.7	0.1	0.1	0.7	0.5	1.8	0.2	1.1	0.4	0.1	0.1	0.1	0.2	0.1	0.0	0.1	0.0	4.1983
0.2	0.2	IkappaB-associated protein	AF153419.2	202490_at	1.3	3.6	2.2	0.4	0.4	0.5	0.5	0.1	0.3	0.0	0.2	0.0	0.3	0.3	0.5	0.5	0.2	0.4	0.2	0.4	0.2	4.1747
4.1	1.5	FLJ21472	NM_024837.1	220416_at	9.1	9.7	12.2	1.9	3.3	3.0	3.0	1.9	0.8	0.6	1.1	0.9	0.7	0.6	0.2	0.8	0.3	0.0	0.3	0.0	0.4	4.1718
1.4	1.3	nemo-like kinase	NM_016231.1	218318_s_at	6.2	7.0	7.1	0.8	0.9	0.8	0.8	0.6	0.5	1.0	0.7	0.7	1.6	1.3	0.9	1.2	1.1	0.4	1.1	0.4	4.1558	
0.1	0.1	FLJ14135 fis; clone MAMMA1002728	AW166925	215201_at	2.1	3.5	5.1	0.5	0.7	0.8	0.8	0.9	0.0	0.1	0.1	0.1	0.5	0.3	0.8	0.4	0.5	0.1	0.1	0.1	4.1491	
0.6	1.4	ETS2 intronic transcript 1 mRNA	AV700891	222303_at	31.1	86.8	63.8	3.6	2.2	2.9	2.9	3.2	10.8	10.5	16.6	19.0	12	0.7	0.7	8.1	0.3	0.8	0.3	0.8	4.0555	
2.8	5.0	DKFZp434F205	AL136877.1	201664_at	173	27.7	31.8	4.4	5.3	9.1	9.1	8.3	4.3	3.9	5.7	5.5	0.1	4.8	4.2	2.5	4.1	4.8	4.1	4.8	3.8471	
5.6	4.6	MAP-kinase activating death domain	AB002356.1	210252_s_at	12.7	35.0	40.7	6.2	6.1	7.0	7.0	8.3	2.2	1.3	1.9	3.3	5.2	2.7	5.4	3.0	3.5	1.1	3.5	1.1	3.8424	
1.7	0.1	y-ets avian erythroblastosis virus E26	AL575509	201328_at	184	34.7	50.7	2.8	1.6	1.7	1.7	1.8	6.4	9.9	8.7	8.9	0.5	0.9	1.0	4.4	0.1	1.7	0.1	1.7	3.8075	
1.2	1.0	oncogene homolog 2	NM_022754	218392_x_at	3.5	7.5	7.4	1.4	1.0	2.7	2.7	1.5	1.0	0.6	0.9	0.1	0.9	1.4	0.4	0.7	0.5	1.4	0.5	1.4	3.7693	
0.0	0.3	FLJ14150 fis; clone MAMMA1003026	NM_001813.1	205046_at	1.5	8.1	13.1	1.7	0.5	1.9	1.9	1.2	0.5	1.3	1.0	0.9	1.1	1.5	0.9	1.0	0.4	0.2	0.4	0.2	3.7324	
0.6	0.8	histamine H4 receptor	AF312230.1	221170_at	35.9	34.2	32.5	7.8	11.9	8.7	8.7	9.3	0.2	0.8	0.8	1.0	0.4	0.8	0.5	0.6	0.0	0.1	0.0	0.1	3.6719	
2.2	4.3	chromosome-associated polypeptide C	NM_005496.1	201663_s_at	17.6	15.1	18.1	3.4	6.6	4.9	4.9	4.2	4.0	3.7	2.2	2.7	1.7	4.1	2.9	1.7	3.7	4.2	3.7	4.2	3.6472	
11.8	4.9	lectin, galactoside-binding, soluble, 8	AL659005	208933_s_at	26.7	28.3	28.2	5.9	6.6	10.1	10.1	4.8	3.8	4.5	5.5	2.1	4.3	7.6	7.4	7.2	4.3	2.7	4.3	2.7	3.6311	
50.4	38.9	(galectin 8)	AL563460	209710_at	141.1	189.2	154.7	4.4	1.3	3.8	3.8	3.1	0.7	1.2	5.4	10.8	2.5	0.7	0.9	0.3	0.1	6.3	0.1	6.3	3.6251	
3.3	2.5	GATA-binding protein 2	NM_003645.1	205769_at	7.0	16.2	9.2	0.3	0.3	0.3	0.3	0.5	0.1	0.4	0.2	0.3	0.2	0.4	0.7	0.1	0.1	0.3	0.1	0.3	3.5389	
8.4	2.6	long-chain 1 (FACVL1)	D86962.1	209409_at	12.5	38.0	33.1	4.9	4.2	12.3	12.3	10.4	1.7	1.7	2.1	1.8	1.4	0.4	0.4	0.7	1.5	0.4	4.8	0.4	3.4907	
5.5	4.1	KIAA0207	AB002356	38398_at	13.8	24.6	29.8	6.1	6.4	5.6	5.6	7.0	3.0	3.2	3.3	4.1	5.1	3.3	5.3	3.7	4.4	2.5	4.4	2.5	3.4534	
5.6	3.6	KIAA0358	NM_003914.1	205899_at	16.2	20.6	10.5	0.1	0.6	0.9	0.9	0.1	1.6	0.1	0.8	0.4	1.9	0.7	0.1	0.1	0.1	0.3	0.8	0.3	3.3824	
8.2	5.3	cyclin A1	NM_012097.1	218150_at	37.6	56.6	54.6	9.1	8.6	14.0	14.0	12.1	3.9	5.0	7.7	9.6	3.8	8.3	8.1	14.5	9.9	8.1	9.9	8.1	3.3745	
2.1	1.8	ADP-ribosylation factor-like 5	A1338837	213097_s_at	8.4	13.4	16.7	4.8	2.1	4.8	4.8	3.7	1.8	1.2	1.2	1.6	0.3	3.4	3.7	2.3	2.3	3.3	2.8	3.3	3.3672	
1.2	2.3	zuotin related factor 1	NM_018030.1	208158_s_at	8.8	18.0	15.3	0.6	0.8	1.6	1.6	1.4	1.5	2.3	2.7	1.8	2.0	0.2	0.7	1.3	0.5	4.0	0.5	4.0	3.342	
1.2	0.7	oxysterol-binding protein-related protein	AF191492.1	210109_at	3.6	6.4	4.2	1.2	1.6	1.0	1.0	0.3	0.6	1.1	1.7	0.6	0.2	1.3	0.5	1.4	0.6	0.1	0.6	0.1	3.2977	
1.0	1.1	nasopharyngeal carcinoma associated gene protein-8	NM_025143.1	220918_at	26.1	37.3	26.2	6.2	6.5	14.1	14.1	11.3	3.3	2.5	2.0	2.0	1.1	0.9	0.9	3.5	1.1	0.1	1.1	0.1	3.2902	
1.2	0.1	aml 1 (acute myeloid leukemia 1)	L34598.1	209359_x_at	3.1	7.2	7.1	2.5	1.6	1.6	1.6	1.1	0.2	1.0	0.6	1.4	0.7	0.7	0.7	1.0	0.8	0.6	0.1	0.1	3.2789	
3.6	7.6	oncogene	NM_030941.1	208107_s_at	7.8	30.6	20.1	1.6	2.3	2.7	2.7	0.8	0.6	0.2	1.5	1.0	0.2	0.1	0.3	0.2	0.1	1.2	0.1	1.2	3.2356	
18.2	16.2	exonuclease NEF-sp	AV715767	212412_at	41.3	72.5	67.3	7.7	7.7	16.3	16.3	11.6	6.4	6.3	9.1	12.7	3.7	3.1	4.1	8.0	3.3	18.3	3.3	18.3	3.2017	
2.9	2.5	DKFZp564A072	AC004381	215215_s_at	4.8	12.8	10.4	0.6	0.9	1.4	1.4	0.8	0.1	0.0	0.2	0.8	0.1	0.4	0.3	0.4	0.3	0.5	0.3	0.5	3.198	
7.6	5.4	chromosome 16 BAC clone	AB014731.1	221509_at	13.2	48.5	32.4	5.2	5.7	18.1	18.1	10.7	3.5	3.8	11.4	8.1	2.8	5.6	6.0	4.1	7.5	8.0	7.5	8.0	3.1618	
1.3	2.4	CIT9875K-44M2	NM_018439.1	218637_at	2.9	10.7	9.3	1.5	1.5	2.7	2.7	2.1	0.6	0.7	0.6	0.6	1.2	0.8	0.7	0.9	0.9	1.1	1.1	2.1	3.1587	
0.8	0.5	SMAP-3	NM_018191.1	218352_at	4.9	13.7	8.7	2.3	1.7	3.4	3.4	3.9	1.0	2.0	2.8	3.6	0.8	2.3	2.0	1.7	2.2	2.4	2.2	2.4	3.1058	
2.1	3.8	hypothetical protein IMPACT	A1081194	213035_at	11.1	26.7	22.4	2.5	1.5	3.4	3.4	2.5	1.9	1.1	2.3	1.6	4.6	2.5	1.3	0.1	0.1	2.2	6.1	3.0937		
1.5	0.2	hypothetical protein FLJ10716	D89788.1	211180_x_at	3.1	9.4	7.5	2.0	2.5	1.7	1.7	1.7	1.0	1.4	0.3	1.1	0.4	0.4	0.6	1.1	0.7	0.2	0.7	0.2	3.0936	
2.1	1.1	aml 1 (acute myeloid leukemia 1) oncogene	AL136105	210731_s_at	4.8	9.1	6.4	1.9	1.8	3.0	3.0	1.8	1.2	1.4	2.7	1.6	2.1	1.2	1.2	1.2	1.7	1.3	0.9	1.3	3.0876	
2.3	1.9	lectin, galactoside-binding, soluble, 8	BE464756	2203164_at	3.7	12.6	12.4	2.5	1.9	4.0	4.0	2.7	1.1	0.6	1.2	1.7	1.4	2.3	2.6	2.1	2.7	2.5	2.7	2.5	3.063	
3.0	1.7	acetyl-Coenzyme A transporter	NM_003645.1	205768_s_at	3.9	10.7	7.7	0.4	0.1	0.6	0.6	0.2	0.1	0.8	0.1	0.7	0.0	0.8	0.1	0.2	0.2	0.1	0.1	0.1	3.0353	
25.1	4.9	fatty-acid-Coenzyme A ligase, very	AB003476.1	210517_s_at	44.0	69.5	59.6	1.5	0.4	0.6	0.6	0.8	0.1	0.2	1.0	3.0	0.9	0.8	0.5	0.1	0.7	0.3	0.3	18.8	3.0146	
2.3	1.1	long-chain 1 (FACVL1)	AF102988.1	210647_x_at	18.7	13.2	9.1	3.4	3.3	4.0	4.0	4.5	3.3	5.0	4.2	3.6	1.8	3.5	4.4	1.8	2.8	2.8	2.8	2.2	3.002	

Fig. 6B

B. Eosinophil (Eo)-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC																				Fb	FoSL		
			cord blood	lung	MC	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	CD4	CD8	CD14	CD19						
207328_at	NM_001140.1	15-lipoxygenase	0.1	0.6	0.7	0.1	0.1	0.1	14.5	24.6	18.3	17.0	0.1	1.1	0.1	0.1	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.1	0.0	74.129
219695_at	NM_024703.1	FLJ22593	0.0	1.0	1.8	1.8	1.1	29.8	34.7	24.8	27.8	0.8	1.5	0.4	0.9	0.1	0.6	0.4	0.3	0.1	0.1	0.1	0.1	0.1	0.1	19.123
208253_at	NM_014442.1	sialic acid binding Ig-like lectin, Sigtec B	1.3	2.4	0.4	0.4	0.2	17.1	23.1	17.6	11.8	0.1	0.4	0.1	0.8	0.3	0.2	0.1	0.2	0.5	0.2	0.5	0.2	0.2	0.2	98056
211922_s_at	AY028632.1	catalase	3.7	2.2	6.2	6.8	2.2	78.2	134.5	119.7	88.8	16.2	13.0	8.8	8.7	0.7	2.2	2.9	11.1	7.5	4.6	9.125				9.125
201802_at	NM_004955.1	solute carrier family 29 (nucleoside transporters)	4.8	2.8	2.9	3.4	1.9	24.8	30.4	36.1	42.3	0.1	0.6	0.6	0.8	0.2	0.9	0.3	2.2	1.0	1.1	8.989				8.989
214523_at	NM_001805.1	CCAAT enhancer binding protein (CEBP), epsilon	0.1	0.1	0.7	1.2	1.2	7.9	11.4	23.4	17.3	1.8	1.5	1.9	1.1	1.4	0.5	0.4	1.0	0.1	0.1	8.9462				8.9462
210029_at	M34455.1	interferon-gamma-inducible indoleamine 2,3-dioxygenase	0.7	0.1	5.3	4.2	2.6	20.0	39.0	33.4	29.5	1.6	2.1	2.3	1.8	1.7	1.5	1.7	0.3	1.4	0.9	7.7078				7.7078
215573_at	AU147084	FLJ12072	0.1	0.1	0.5	0.3	1.1	9.8	8.4	16.9	7.2	0.4	1.9	1.8	2.0	0.1	0.1	0.0	0.1	0.4	0.0	7.5983				7.5983
201801_s_at	AF079117.1	solute carrier family 29 (nucleoside transporters)	3.5	1.9	1.7	0.5	0.9	29.7	47.1	7.4	11.0	0.1	0.5	0.4	0.7	1.1	0.4	0.1	1.4	0.6	1.0	7.0314				7.0314
213825_at	AF221520.1	oligodendrocyte lineage transcription factor 2	0.4	0.6	0.2	0.4	0.6	6.0	10.9	18.7	12.5	0.8	0.9	1.5	1.0	0.6	1.7	0.3	0.4	0.3	0.3	6.5987				6.5987
219821_s_at	NM_018988.1	glucose-fructose oxidoreductase domain containing	3.0	1.4	1.8	2.6	2.3	18.7	17.3	30.9	31.3	3.9	3.1	2.4	2.9	3.2	1.3	2.5	3.0	3.8	0.8	6.2284				6.2284
205472_s_at	NM_004392.1	dachshund (Drosophila) homolog	0.0	0.1	0.1	0.4	0.1	2.7	1.4	2.2	1.7	0.3	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.3	0.0	6.0088				6.0088
202188_at	NM_014669.1	KIAA0095	0.5	0.9	0.4	1.8	1.2	6.8	8.5	13.5	10.6	0.2	0.2	0.2	0.1	0.2	0.3	1.7	1.7	1.4	0.4	5.4499				5.4499
210548_at	U58913.1	chemokine CCL23	0.6	1.8	0.4	1.1	0.5	5.5	6.2	4.2	6.9	0.1	0.9	0.1	0.2	0.3	0.1	0.2	0.6	0.1	0.0	5.3082				5.3082
209447_at	AF043290.1	lymphocyte membrane associated protein (887)	0.6	0.5	2.5	3.4	3.6	41.8	49.7	66.2	60.1	0.2	0.9	0.5	1.2	2.6	5.1	10.4	1.6	6.3	2.7	5.1472				5.1472
206171_at	NM_000677.2	ADORA3 adenosine A3 receptor	2.3	2.8	2.8	3.7	2.2	7.8	13.9	22.0	17.9	1.6	3.1	2.2	2.5	1.2	1.6	0.5	2.0	0.5	0.5	5.0469				5.0469
210549_s_at	U58913.1	chemokine CCL23	1.1	1.1	0.1	1.3	0.6	7.9	5.6	2.7	8.1	0.0	0.6	0.0	0.2	0.1	0.1	0.1	0.2	0.0	0.4	4.9873				4.9873
214183_s_at	X91817.1	transketolase-like protein	0.1	0.2	0.2	0.1	0.1	3.2	4.0	6.6	7.2	0.2	0.2	0.1	0.1	0.2	0.2	1.0	0.1	0.6	0.0	4.7894				4.7894
215350_at	AB033088.1	spectrin repeat containing, nuclear envelope 1	0.1	0.1	0.5	0.1	0.1	3.8	4.2	3.0	2.8	0.0	0.1	0.2	0.4	0.7	0.2	0.1	0.0	0.1	0.2	4.7822				4.7822
206277_at	NM_002564.1	P2Y2 purinergic receptor	0.1	0.1	0.1	0.2	0.1	3.4	4.7	8.1	5.9	0.1	0.3	0.1	0.1	0.2	0.1	0.3	1.2	0.2	0.1	4.3043				4.3043
204776_at	NM_003248.1	thrombospondin 4 (THBS4)	0.8	0.1	1.5	0.1	0.8	3.2	5.9	10.0	6.4	1.8	1.4	0.6	0.9	0.3	0.2	0.3	1.4	1.1	1.2	4.1746				4.1746
201563_at	L29008.1	L-kidol-2 dehydrogenase	4.1	2.6	3.5	11.4	12.8	22.5	29.9	49.0	37.0	1.8	3.0	4.4	2.2	2.1	1.6	1.2	2.7	2.5	1.8	4.1557				4.1557
206637_at	NM_014879.1	P2YX purinergic receptor GPR105 for UDP-glucose	5.7	1.6	13.3	19.9	13.5	44.2	55.1	81.4	62.4	1.8	9.3	15.4	9.2	0.7	0.9	0.8	0.0	5.5	0.1	3.8761				3.8761
213622_at	A1733465	collagen, type IX, alpha 2	1.5	1.4	1.9	1.2	1.3	10.3	9.6	6.6	8.8	2.7	2.1	2.1	2.2	0.7	1.2	1.2	2.2	1.7	0.9	3.8576				3.8576
214705_at	AJ001306.1	PDZ domain protein	0.1	0.1	0.4	0.3	0.1	2.1	1.5	2.6	2.2	0.3	0.0	0.6	0.7	0.1	0.4	0.3	0.3	0.6	0.1	3.6532				3.6532
266_s_at	L33930	CD24 signal transducer	0.2	0.1	3.0	0.3	0.8	11.9	14.0	18.8	13.9	0.1	0.1	0.3	0.8	0.9	0.0	0.1	0.1	0.4	0.2	3.3793				3.3793
201432_at	NM_001752.1	catalase (CAT)	23.0	14.3	35.7	49.4	19.9	202.3	209.7	221.6	207.3	67.0	54.3	71.3	60.9	9.2	11.2	15.1	53.6	29.9	21.4	3.3325				3.3325
209696_at	D26054.1	fructose-1,6-bisphosphatase	0.9	3.4	4.3	11.1	6.4	20.2	27.7	28.8	32.5	3.0	2.5	2.4	1.5	1.9	2.0	1.6	8.1	1.1	0.6	3.3089				3.3089
216379_x_at	AK000168.1	CD24 signal transducer	1.3	1.4	16.2	0.9	1.5	66.1	70.1	81.9	77.9	1.7	2.8	2.6	4.1	4.8	0.5	0.6	0.9	22.5	0.5	3.2741				3.2741
205569_at	NM_014398.1	lysosome-associated membrane glycoprotein (TSC403)	0.4	0.2	0.7	0.1	0.4	2.4	3.1	6.8	3.0	0.6	0.1	1.4	0.8	0.4	1.1	0.7	0.1	0.0	0.3	3.2308				3.2308
219233_s_at	NM_018530.1	hypothetical protein PRO2521	0.1	1.9	2.1	4.6	5.4	7.5	8.5	21.8	21.2	0.8	0.1	1.5	2.1	0.1	1.1	4.1	0.1	1.4	0.5	3.2093				3.2093
202286_s_at	J04152	gastrointestinal tumor-associated antigen GA733-1	0.9	0.7	1.3	0.3	0.1	1.1	2.5	8.7	1.8	0.4	0.8	0.6	0.6	0.2	0.2	0.7	0.3	0.5	0.1	3.1844				3.1844
206442_at	NM_003007.1	semenogelin I (SEMGI)	0.6	0.1	0.4	0.0	0.1	1.2	3.2	4.9	3.4	0.3	0.2	1.1	1.9	0.1	0.2	0.2	0.9	0.4	0.1	3.1837				3.1837
205733_at	NM_000057.1	Bloom syndrome	1.9	1.1	2.0	2.4	2.2	8.5	6.0	7.5	11.2	2.1	2.0	1.0	1.2	1.2	2.4	1.8	1.1	2.6	1.2	3.1427				3.1427
204392_at	NM_003656.2	calcium/calmodulin-dependent protein kinase I (CAMKI)	4.0	1.1	6.3	8.9	6.4	17.8	19.3	24.9	26.5	0.6	0.2	1.8	1.5	0.1	1.4	1.0	3.0	0.6	1.8	3.0763				3.0763
213497_at	AL050374.1	DKFZp586C1619	1.0	0.7	1.0	1.3	1.6	6.3	6.8	6.8	6.0	2.3	3.0	1.4	2.3	2.0	0.4	0.5	1.6	1.1	0.8	3.0099				3.0099
219296_at	NM_019028.1	similar to ankyrin repeat-containing protein AKR1	2.2	1.7	0.2	3.5	1.6	7.3	4.4	8.4	7.4	1.8	2.4	2.4	2.3	0.1	1.4	1.6	1.3	1.9	0.8	3.0018				3.0018

Fig. 6C

C. Neutrophil (Ne)-selective transcripts (1/7).

Probe set	Accession #	Transcripts	MC														NeSL																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
			cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo1 (small)	Eo2 (small)	Eo3 (small)	Eo4 (small)	Ne1 (small)	Ne2 (small)	Ne3 (small)	Ne4 (small)																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
205403_at	NM_004633.1	interleukin 1R, type II	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	

Fig. 6D

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C. Neutrophil (Ne)-selective transcripts (2/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pI	CD4	CD8	CD14	CD19	Fb	NeSL
210789_x_at	U0692.1	carcinoembryonic antigen (CGM1)	1.1	0.4	1.9	1.4	1.5	2.0	1.5	2.5	0.4	1.94	18.6	22.6	15.5	0.7	1.6	0.9	2.0	0.3	1.1	9.2749
210772_at	M88107.1	formyl peptide receptor 2	0.1	0.2	0.4	0.7	0.7	0.7	0.3	0.8	0.7	51.4	67.7	44.8	46.4	0.5	0.5	0.5	5.6	0.1	0.1	9.2661
218978_s_at	NM_018586.1	PRO1584	0.7	0.5	1.6	0.2	0.5	1.1	0.9	0.7	0.5	26.3	20.5	6.6	2.8	0.2	0.7	0.4	1.1	0.2	0.4	9.1536
204006_s_at	NM_000570.1	R Fc gamma R IIb (CD16)	0.7	0.2	1.2	0.7	0.6	0.7	0.8	0.0	0.7	230.7	278.8	47.6	45.9	4.2	1.9	6.9	12.0	3.9	0.1	9.0769
207275_s_at	NM_001995.1	fatty acid-Coenzyme A ligase, long-chain 1 (FACL1)	4.3	2.6	5.1	11.5	19.4	5.3	5.1	5.9	3.7	93.8	127.8	92.8	69.1	0.7	1.0	1.1	8.3	0.9	1.7	8.9855
220302_at	NM_005906.2	male germ cell-associated kinase	0.1	0.0	1.3	0.7	0.8	0.7	0.2	2.0	1.4	7.9	8.4	7.9	8.9	0.3	0.1	0.0	0.1	0.1	0.0	8.866
221803_s_at	AA883074	nuclear receptor binding factor-2	1.1	0.8	3.2	4.0	2.9	2.8	2.8	4.7	3.2	24.7	25.2	33.2	29.3	0.1	1.5	1.2	1.7	2.0	2.6	8.3788
206765_at	AF153820.1	KCNJ2 inwardly-rectifying potassium channel Kir2.1	1.0	0.4	2.5	4.4	4.4	2.4	4.7	6.1	8.0	25.8	36.2	52.4	48.3	0.4	0.2	0.5	1.5	0.7	1.1	8.108
213351_s_at	A1934469	KIAA0779	0.0	0.1	0.9	2.0	1.6	0.8	0.6	2.3	2.7	7.9	5.9	20.1	18.0	0.2	0.5	0.2	0.1	0.2	1.2	7.9705
214590_s_at	AL545760	ubiquitin-conjugating enzyme E2D1 leukotriene B4 omega hydroxylase (CYP4F3)	0.1	1.5	0.3	0.4	0.5	1.1	1.0	0.5	0.4	7.9	10.7	10.1	4.4	0.1	0.4	0.3	1.0	0.4	0.9	7.8712
206522_at	NM_004668.1	R Fc gamma receptor IIc2	0.0	0.0	0.8	1.8	1.0	3.0	5.4	11.7	9.4	46.0	51.5	56.9	43.0	0.1	0.0	0.0	0.6	0.6	0.1	7.5773
210992_x_at	U90939.1	VNN3 protein	1.9	1.0	1.7	2.1	3.3	8.1	16.1	2.8	4.2	70.9	95.6	42.8	30.5	0.3	0.2	0.1	7.2	2.3	0.2	7.5239
220528_at	NM_018399.1	early development regulator 2	0.1	0.2	1.3	6.1	5.0	0.2	0.1	0.5	0.4	26.8	22.1	20.0	36.8	0.8	0.2	0.1	3.0	0.1	0.1	7.5216
200919_at	NM_004427.1	glycerol kinase	5.6	4.4	4.8	6.5	9.6	7.6	6.8	5.3	7.3	109.5	89.0	52.9	61.4	2.5	4.9	7.0	10.0	3.9	6.5	7.5056
207387_s_at	NM_000167.1	heat-shock protein HSP70B	2.1	1.5	1.0	1.5	1.6	1.1	1.4	1.6	1.4	14.3	20.3	10.7	10.3	0.9	0.6	0.3	1.7	0.6	0.6	7.4603
117_at	X51757	glutaminyl-peptide cyclotransferase	1.1	0.2	0.8	0.6	0.9	5.9	8.3	2.1	4.1	46.3	41.2	25.1	25.8	0.4	0.9	0.6	3.7	1.6	0.5	7.4139
205174_s_at	NM_012413.2	triggering receptor expressed on myeloid cells 1	0.4	0.0	0.4	0.7	0.9	0.7	0.0	0.4	0.3	30.1	47.7	36.4	24.7	0.7	0.6	0.0	4.6	0.1	1.5	7.3246
219434_at	NM_018643.1	thrombomodulin	1.3	0.3	0.4	0.2	0.5	2.9	0.7	1.4	1.5	92.8	84.0	81.2	98.6	3.4	0.6	0.1	12.3	0.9	0.3	7.2368
203887_s_at	NM_000361.1	orosomucoid 1 (ORM1)	1.7	0.1	0.4	0.4	0.4	0.2	1.0	1.4	1.1	16.8	13.0	13.4	1.3	0.7	0.6	0.4	1.1	0.4	0.2	7.1328
205040_at	NM_000607.1	glycerol kinase	0.5	0.1	0.1	0.4	0.1	0.1	0.0	1.1	0.0	3.4	4.1	4.3	0.7	0.1	0.3	0.1	0.4	0.0	0.2	7.0823
214681_at	A1830490	FLJ20273	0.2	0.4	0.1	1.2	1.7	0.8	1.1	0.6	1.2	7.8	14.2	24.0	12.1	0.9	0.0	0.1	1.9	1.0	0.3	6.966
218035_s_at	NM_019027.1	GTPase regulator associated with the focal adhesion kinase pp125(FAK)	2.9	1.0	0.9	1.5	0.8	0.9	0.4	1.3	1.1	47.2	54.4	91.9	94.0	1.7	0.7	0.4	9.9	1.5	0.3	6.9074
205068_s_at	BE671084	secretory leukocyte protease inhibitor (antileukoprotease) (SLPI)	1.2	1.4	3.5	5.9	5.1	6.5	5.1	8.5	7.1	43.7	40.6	45.2	56.0	0.7	1.3	2.9	5.1	0.8	1.2	6.8934
203021_at	NM_003064.1	glycerol kinase pseudogene, chromosome 1	1.7	0.8	4.6	1.5	1.1	1.2	2.2	8.5	0.8	16.2	19.8	13.9	8.7	1.8	0.6	1.2	1.7	1.1	2.1	6.7497
216316_x_at	X78713	carcinoembryonic antigen subdomains A and B	2.0	0.9	0.4	0.6	1.0	0.7	0.6	0.5	1.0	10.3	18.6	5.8	5.8	0.5	0.2	0.2	0.8	0.3	0.1	6.6675
217209_at	X16454	FLJ21458	0.6	0.4	0.2	0.2	0.4	0.1	0.3	0.7	0.5	2.8	3.8	3.3	2.7	0.3	0.4	0.0	0.1	0.1	0.2	6.5382
220421_at	NM_024850.1	putative lymphocyte G0G1 switch gene (G0S2)	0.3	0.6	0.1	0.1	0.1	0.3	0.8	0.4	0.3	8.9	7.2	9.1	7.0	1.2	0.6	0.0	0.1	0.1	0.2	6.4857
213524_s_at	NM_015714.1	transducin-like enhancer of split 3	0.8	0.8	1.3	0.9	0.5	8.0	8.5	18.7	10.1	118.0	52.0	39.6	92.5	1.7	0.8	0.1	6.0	0.2	3.4	6.4779
206472_s_at	NM_005078.1	KIAA1547	2.2	2.6	1.3	0.7	0.5	1.6	0.6	0.5	1.0	22.6	25.0	11.3	8.3	1.3	1.2	1.5	1.8	1.5	0.9	6.4334
212769_at	AI557426	KIAA0329	1.4	1.5	0.5	1.3	2.3	1.1	1.0	2.2	1.9	17.9	15.9	15.1	12.8	2.4	0.8	1.1	1.3	1.2	0.5	6.4271
204307_at	AB002295.1	granulocyte colony-stimulating factor receptor	0.7	0.0	0.1	2.6	2.1	1.8	1.5	2.4	2.0	10.3	11.2	15.4	12.8	1.9	0.1	0.5	0.2	0.1	0.5	6.3478
203591_s_at	NM_000760.1	R immunoglobulin superfamily member WM78	0.1	0.0	1.0	0.1	0.2	2.3	0.6	2.4	1.0	220.3	187.2	134.9	112.1	0.2	0.8	0.2	25.5	0.1	0.2	6.2051
210210_at	AF181660.1	FLJ11151	0.9	1.1	1.6	1.8	1.9	1.1	1.9	1.7	2.0	11.1	7.0	13.7	14.1	1.4	1.3	0.9	1.6	1.1	0.6	6.172
218610_s_at	NM_018340.1	R Fc gamma receptor IIa (CD32)	1.5	1.2	1.2	1.2	1.8	3.3	3.2	2.6	1.8	25.2	23.3	17.9	21.8	0.5	0.6	0.4	3.6	0.4	0.6	6.112
203561_at	NM_021642.1	superoxide dismutase 2	4.7	1.2	0.9	1.2	2.4	19.5	22.8	19.4	21.4	104.3	129.0	153.0	123.9	4.0	0.7	0.7	16.3	2.2	0.2	6.1015
216941_s_at	X15132.1		1.3	1.1	1.2	1.8	2.2	1.4	1.3	3.2	2.4	20.5	44.6	35.8	42.2	5.6	0.8	0.7	2.0	0.7	1.1	6.0724

Fig. 6E

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C. Neutrophil (Ne)-selective transcripts (3/7).

C. Neutrophil (Ne)-selective transcripts (3/7).																						
Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ne.SI.
207624_s_at	NM_000328.1	retinitis pigmentosa GTPase	0.0	0.6	1.1	2.0	1.2	1.1	1.2	2.1	2.8	7.1	7.0	13.6	15.1	0.2	1.2	0.4	0.9	0.7	0.3	60348
209850_s_at	BC005406.1	regulator (RPGR)	0.2	0.2	1.3	0.2	1.0	0.2	0.4	0.5	0.4	13.2	9.6	6.7	8.7	0.2	0.2	0.2	0.6	0.4	1.6	59313
203936_s_at	NM_004994.1	Cdc42 effector protein 2	47.7	0.6	1.6	1.9	1.4	1.2	2.4	15.5	1.5	36.5	35.1	36.8	21.9	1.7	2.0	1.4	1.9	1.3	1.4	59311
215966_x_at	AA292874	matrix metalloproteinase 9 glyceral kinase	1.2	0.2	0.6	0.1	1.2	0.2	1.0	1.2	1.2	6.6	10.2	7.3	7.4	0.2	0.1	0.2	1.3	0.5	0.0	59077
206925_at	NM_005668.1	sialyltransferase 8	3.1	1.2	2.1	2.5	2.0	1.4	3.1	1.6	1.6	21.7	33.3	6.8	11.4	0.4	0.9	1.6	2.6	1.2	0.2	58688
211764_s_at	BC005980.1	ubiquitin-conjugating enzyme E2D 1 phosphotidylinositol transfer protein (PITPN)	1.8	1.4	1.1	2.9	2.4	7.5	5.7	3.9	2.2	29.3	31.2	52.6	25.4	0.2	2.0	1.4	5.7	1.3	2.3	58143
201192_s_at	NM_006224.1	placental taurine transporter	3.0	3.1	1.9	5.0	4.6	3.9	5.4	6.6	5.4	27.9	26.9	32.9	35.2	2.0	3.5	3.7	5.0	3.2	2.8	5811
205921_s_at	U16120.1	ubiquitin C-terminal hydrolase	1.2	0.7	0.5	0.2	0.4	0.3	1.6	0.5	0.9	14.8	17.2	2.8	2.6	0.0	0.1	0.3	1.1	0.3	0.4	57909
209137_s_at	BC000263.1	related polypeptide	3.6	4.1	2.0	2.6	1.9	1.5	0.9	2.7	0.9	25.0	24.5	37.6	29.7	3.5	5.0	2.5	3.5	2.7	3.0	57864
208052_x_at	NM_001815.1	carcinoembryonic antigen-related cell	1.7	1.4	2.9	2.7	1.9	3.0	2.6	2.8	2.1	14.3	16.5	20.0	13.7	2.5	1.3	2.3	2.8	2.5	1.6	57572
201393_s_at	NM_000876.1	adhesion molecule 3 (CEACAM3)	6.4	2.8	0.2	0.8	1.8	4.1	5.4	6.8	5.4	82.4	106.9	80.1	71.7	1.7	2.9	8.7	8.4	4.8	14.8	57104
218614_at	NM_018169.1	insulin-like growth factor 2 receptor	1.2	1.0	6.9	13.7	12.5	3.2	3.3	7.7	5.8	52.7	54.4	82.8	83.3	2.9	8.7	11.8	3.2	10.8	1.3	56442
202084_s_at	NM_003003.1	FLJ10652	5.7	2.5	12.8	28.8	22.6	20.6	18.7	35.5	29.5	130.7	129.7	135.6	177.9	19.2	4.1	3.5	11.5	7.7	11.8	56423
32069_at	AB014515	SEC14 (S. cerevisiae)-like 1	2.8	1.5	2.1	5.6	5.5	4.6	3.7	5.9	6.9	23.9	20.9	35.1	40.5	1.0	3.4	3.3	2.6	2.1	1.5	56348
205896_at	NM_003059.1	KIAA0615	0.8	1.2	1.0	0.1	1.1	1.9	2.4	3.5	2.7	8.5	13.3	30.0	12.6	0.5	0.7	0.8	2.6	0.5	1.4	54612
206584_at	NM_015364.1	solute carrier family 22, member 4 (SLC22A4)	7.4	1.7	2.0	3.9	1.8	1.0	0.4	0.6	0.5	43.9	62.3	87.8	56.0	1.3	3.5	1.0	11.1	3.5	9.4	54459
202082_s_at	NM_003003.1	MD-2 protein	1.0	0.3	3.6	2.5	2.2	15.5	5.4	12.3	8.4	40.2	57.3	54.9	60.9	3.8	0.8	1.3	2.7	3.3	2.4	54422
204308_s_at	NM_014844.1	SEC14 (S. cerevisiae)-like 1	2.9	1.1	2.2	2.8	2.8	2.1	3.1	3.1	4.3	16.5	18.7	19.9	19.0	3.4	1.3	1.7	1.8	1.3	2.5	54369
207500_at	NM_004347.1	KIAA0329	0.3	1.1	0.1	0.0	0.1	0.1	0.3	0.2	0.5	4.2	6.2	4.6	2.9	0.3	0.3	0.4	0.8	0.1	0.3	5379
203435_s_at	NM_007287.7	caspase 5	0.3	0.5	0.4	0.3	0.2	0.1	0.3	0.3	0.2	16.4	44.2	54.6	42.8	0.2	0.3	0.2	0.2	0.2	6.9	52591
205539_at	NM_006576.1	CD10, membrane	0.4	0.5	2.0	1.4	0.8	1.0	1.1	1.0	1.1	8.4	6.9	6.0	10.1	1.0	1.3	0.4	1.5	0.7	1.1	52541
204601_at	NM_014664.1	metallo-endopeptidase	1.9	1.2	1.3	3.2	2.3	3.0	2.7	3.7	3.0	12.9	12.8	20.2	20.0	0.1	2.2	2.6	1.3	1.9	1.0	52381
201963_at	NM_021122.2	advillin	2.9	2.1	5.0	19.9	33.4	6.6	3.8	10.3	6.1	58.8	86.6	92.2	80.2	0.1	1.1	1.1	10.8	1.5	2.4	52374
207064_s_at	NM_009590.1	KIAA0615	0.7	0.1	0.9	0.9	0.8	0.8	0.8	0.9	1.2	4.3	4.7	4.0	6.6	0.8	0.5	0.8	0.5	0.8	0.3	51905
220005_at	NM_023914.1	fatty-acid-Coenzyme A ligase, long-chain 1 (FACL1)	0.6	0.0	0.1	0.5	0.1	19.7	9.6	25.1	17.3	76.5	77.1	100.7	98.6	1.9	0.1	0.2	12.3	0.6	0.0	51686
211395_x_at	U90940.1	P2YX purinergic receptor GPR86 for UDP-glucose	4.6	0.3	7.3	9.7	15.1	9.7	19.5	4.4	6.6	115.0	140.3	42.9	38.9	3.0	1.4	0.6	14.0	7.2	1.0	51401
201780_s_at	NM_007282.1	Fc gamma receptor IIc3	4.4	2.8	3.5	9.2	6.6	6.8	6.2	8.9	7.1	27.1	36.6	52.5	35.7	0.8	4.1	3.7	7.2	7.2	4.6	51305
209864_at	AB045118.1	ring finger protein 13 (RNF13)	2.8	1.3	4.4	9.2	8.0	13.4	16.9	27.3	22.6	93.2	97.2	100.6	104.2	1.3	1.9	2.9	10.2	2.5	1.0	51047
218319_at	NM_020651.2	GSK-3 binding protein FRAT2	3.4	2.9	5.9	17.5	33.5	17.7	11.7	12.6	15.1	64.9	88.3	73.0	80.2	2.4	6.3	2.9	13.8	12.6	1.1	50403
206632_s_at	NM_004900.1	pellino (Drosophila) homolog 1 (PELL1)	0.6	1.1	1.0	1.2	2.6	1.3	0.8	3.9	0.5	19.6	11.1	30.8	0.5	1.5	0.2	0.4	0.4	1.0	1.2	50277
220990_s_at	NM_030938.1	phorbolin	11.7	6.2	4.6	18.5	12.5	5.0	3.3	8.2	4.9	115.5	117.2	125.3	122.5	2.6	5.3	4.2	24.1	4.4	8.3	49858
221653_x_at	BC004395.1	DKFZp5661133	0.7	2.8	0.6	2.1	1.6	2.0	0.4	1.8	1.1	8.0	3.9	12.7	5.2	0.2	0.9	0.4	1.4	1.1	0.4	49332
204748_at	NM_00963.1	apolipoprotein L	6.5	16.2	0.6	2.4	2.0	4.5	2.3	3.4	3.4	35.8	44.1	44.6	91.8	0.4	0.6	0.2	4.3	0.3	0.5	49206
210423_s_at	L32185.1	COX2 prostaglandin-endoperoxide synthase 2	2.0	0.2	1.4	1.6	1.3	1.3	2.2	1.5	2.0	85.0	78.5	75.2	52.9	1.9	0.4	1.9	14.7	1.0	1.0	48945
206429_at	NM_005242.2	integral membrane protein	0.8	0.8	0.9	0.2	0.9	0.9	1.1	0.2	0.8	11.8	15.1	4.1	4.1	1.3	1.5	0.2	1.5	0.3	0.7	48608
213352_at	A1934469	PAR2 protease-activated receptor-2	0.6	0.9	1.2	1.5	1.2	1.2	1.5	1.5	2.2	8.4	6.0	8.7	7.7	1.6	0.9	1.5	1.0	1.3	0.8	48373
201888_s_at	U81379.3	KIAA0779	0.1	0.6	0.3	0.2	0.0	1.7	2.7	1.7	2.0	8.6	19.0	15.0	13.9	0.4	0.4	0.4	2.9	1.3	1.3	4746
		interleukin-13 receptor																				

Fig. 6F

C. Neutrophil (Ne)-selective transcripts (4/7).

Probe set	Accession #	Transcripts	MC ₁	MC ₂	Ba1	Ba2	Ba3	Eo	Eo	Eo3	Eo4	Ne	Ne	Ne3	Ne4	pl	CD4	CD8	CD14	CD19	Fb	Ba.SI.
204780_s_at	AA164751	CD95, Fas, APO-1	14	14	72	140	115	66	67	93	66	453	388	655	518	13	56	48	36	26	97	47254
209310_s_at	U25804.1	Ich-2 cysteine protease	25	19	21	77	70	14	13	13	14	191	175	367	235	29	41	45	49	39	22	46817
205452_at	NM_004855.1	phosphatidylinositol glycan, class B (PIGB)	23	27	23	64	77	23	14	30	30	163	176	222	393	17	20	29	28	35	22	46577
218298_s_at	NM_024952.1	FLJ20950	31	33	54	81	72	57	57	88	94	372	234	373	391	06	17	31	58	23	27	46558
221210_s_at	NM_030769.1	swineacetylneuraminase lyase	38	12	08	12	14	30	47	32	46	204	236	235	183	06	07	03	46	05	01	46378
221497_x_at	BC005369.1	chromosome 1 open reading frame	30	24	43	57	59	33	76	79	54	293	324	243	215	18	31	29	29	19	20	46333
204668_at	AL031670	12, clone MGC12484	08	05	18	10	12	03	15	17	09	84	81	70	65	14	13	70	75	05	16	4614
201921_at	NM_004125.1	ferritin, light polypeptide-like 1	7.1	54	26	67	65	117	114	208	153	455	875	813	571	08	27	30	84	32	124	45644
209600_s_at	S69189.1	guanine nucleotide binding protein 10 (GNG10)	29	17	28	53	47	14	10	12	13	150	177	214	212	04	10	08	21	07	15	45552
205119_s_at	NM_002029.1	peroxisomal acyl-coenzyme A oxidase	4.1	14	112	266	327	140	11.1	42	60	2882	3158	2747	2529	36	13	07	626	1.1	05	4505
217738_at	BF575514	formyl peptide receptor 1	57	09	74	241	349	75	46	51	39	734	870	899	799	22	17	16	10.1	1.7	28	44839
215078_at	AL050388.1	pre-B-cell colony-enhancing factor	00	07	00	01	04	09	05	08	03	71	129	45	79	01	05	05	1.7	0.1	01	44343
207545_s_at	NM_003744.1	DKFZp564M2422	07	14	11	25	24	27	18	29	12	72	112	105	74	08	05	05	1.6	1.1	12	43728
213418_at	NM_002155.1	numb (Drosophila) homolog	1.1	04	07	15	16	253	288	105	170	1040	916	700	708	05	17	1.1	128	4.7	05	43655
218023_s_at	NM_016605.1	heat shock 70kD protein 6 (HSP70B)	57	38	66	130	126	85	103	130	109	401	397	470	597	30	44	59	70	60	68	43383
210386_s_at	BC001906.1	putative nuclear protein (LOC51307)	62	19	27	54	40	14	22	18	36	195	158	234	238	25	36	26	41	26	47	43318
207643_s_at	NM_001065.1	Similar to metaxin 1	7.8	16	09	73	14	63	74	85	90	81.1	836	686	656	13	22	59	174	06	160	42796
203140_at	NM_001706.1	CD120a, TNF-R1 p55	62	29	91	135	198	235	167	287	33.1	991	1078	1158	101.1	22	34	34	234	6.7	65	42767
207253_s_at	NM_016936.1	B-cell CLL/lymphoma 6 (BCL6)	32	28	29	44	50	38	26	38	36	167	200	142	178	23	25	25	22	24	18	42556
202875_s_at	BE397715	ubiquitin 1	20	14	01	01	02	25	36	21	15	116	154	68	75	08	17	19	1.1	13	07	42425
218791_s_at	NM_024713.1	pre-B-cell leukemia transcription factor 2	12	07	25	27	18	09	15	16	10	69	87	132	112	14	10	05	13	08	12	42174
211862_x_at	AF015451.1	FLJ22557	35	26	168	97	10.1	56	102	77	7.1	657	677	36.1	379	3.1	68	87	10.1	69	20	42001
217986_s_at	NM_013448.1	Usurpin-beta	35	30	35	92	84	61	85	145	13.1	390	351	435	516	25	59	65	70	50	17	41976
217966_s_at	NM_022083.1	bromodomain adjacent to zinc finger domain, 1A	4.1	19	64	74	90	242	148	256	118	519	1053	762	800	09	33	38	32	20	82	41858
212602_at	AI806395	riban	23	35	04	09	1.1	08	06	04	08	17.1	181	129	134	15	05	03	36	08	28	41806
208485_x_at	NM_003879.1	KIAA0993	32	25	192	98	99	62	130	8.1	83	708	697	338	41.4	35	64	84	115	66	20	41719
201942_s_at	D85390.1	CASP8 and FADD-like apoptosis regulator (CFLAR)	06	17	06	13	17	16	70	24	26	159	238	68	81	05	08	13	25	05	26	41525
220933_s_at	NM_024617.1	gp 180-carboxypeptidase D-like enzyme	2.1	20	96	142	140	71	72	109	125	381	373	815	578	19	31	48	62	38	30	41025
221764_at	AL574186	FLJ13409	63	44	165	186	150	104	158	219	227	809	992	463	603	95	89	94	57	94	25	40745
207446_at	NM_006068.1	glycerol-3-phosphate dehydrogenase	05	05	07	15	08	08	09	12	08	76	118	72	87	01	09	09	2.1	12	06	40697
219748_at	NM_024807.1	Toll-like receptor 6	02	03	03	04	06	19	26	16	16	91	91	67	64	02	03	06	05	1.1	00	40619
220945_x_at	NM_018050.1	chromosome 6 open reading frame 76	10	14	05	07	07	17	06	15	10	80	108	136	110	1.1	05	03	09	06	26	4057
212577_at	AA868754	FLJ10298	1.9	13	64	80	99	10.1	240	8.1	94	740	986	422	574	44	108	95	75	160	32	40417
221732_at	AK026161.1	RIKEN cDNA 5830420C20	28	07	34	105	88	50	60	107	109	276	316	308	347	03	04	18	25	16	46	4041
205986_at	NM_004920.1	apoptosis-associated tyrosine kinase	16	13	07	10	05	03	03	14	10	105	158	133	152	32	10	05	34	09	04	40322
213501_at	T62985	acyl-Coenzyme A oxidase 1,	13	11	20	26	28	13	09	12	06	85	115	124	75	01	1.1	03	18	05	1.1	40194
204542_at	NM_006456.1	palmitoyl sialyltransferase (ST6M)	04	02	15	03	02	34	39	45	32	130	134	210	134	07	07	03	14	03	06	4016

Fig. 6G

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C. Neutrophil (Ne)-selective transcripts (5/7).

Probe set	Accession #	Transcripts	MC: cord blood	MC: lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	EO 1	EO 2	EO3 (small)	EO4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	p1 CD4	CD8	CD14	CD19	Fb	NeSL
204071_s_at	NM_005802.1	tumor protein p53-binding protein	14	16	1.1	30	29	3.7	2.3	26	22	10.5	128	80	11.9	1.5	2.2	2.2	2.2	2.1	4.0148
210594_x_at	AF239756.1	myelin protein zero-like 1	12	0.5	0.6	1.5	1.2	0.1	0.4	0.8	1.9	15.3	13.9	7.1	10.9	0.3	0.2	0.6	0.7	2.8	3.9778
203063_at	NM_014634.1	protein phosphatase 1F (pp2C domain containing)	0.5	0.4	1.4	3.3	3.0	4.0	6.0	6.1	10.0	33.1	22.2	29.6	31.8	0.3	2.9	1.2	7.3	1.5	3.9764
201392_s_at	BC031974	insulin-like growth factor 2 receptor	1.7	0.7	0.1	0.0	0.1	2.6	3.0	1.9	1.5	51.1	59.1	12.8	15.0	1.1	1.2	4.0	3.8	2.2	3.9602
221477_s_at	BF575213	MGC5618	2.9	1.4	3.4	4.3	9.0	4.2	4.2	4.2	4.2	56.8	63.6	36.1	46.6	7.9	3.2	1.2	12.6	2.7	3.9562
206756_at	NM_019886.1	carbohydrate (N-acetylglucosamine 6-O)sulfotransferase 7	0.2	0.1	0.1	0.0	0.1	0.1	0.1	0.1	0.1	5.0	3.9	3.5	10.5	0.1	1.3	1.0	1.0	0.2	3.9516
204994_at	NM_002463.1	myxovirus (influenza) resistance 2 (MX2)	1.3	2.3	5.4	7.8	8.2	9.2	11.6	15.2	12.3	49.8	46.6	77.6	80.8	2.4	7.5	6.0	15.6	4.8	3.9478
201943_s_at	NM_001304.2	carboxypeptidase D	0.9	0.9	0.5	2.1	3.6	1.7	7.6	7.2	4.6	16.4	21.3	18.7	15.2	0.7	1.0	1.7	3.3	0.4	3.8926
216252_x_at	Z70519.1	CD95, Fas, APO-1	0.3	0.8	4.3	2.5	1.1	1.8	4.7	1.8	1.7	18.5	31.2	10.3	8.4	2.2	3.8	2.4	1.9	1.4	3.8691
203066_at	NM_014863.1	B cell RAG associated protein (BRAG)	1.3	3.9	0.9	1.2	1.0	10.6	10.2	13.1	20.2	57.0	65.9	95.2	86.9	1.9	0.1	0.0	19.3	4.2	3.8667
212479_s_at	AL050139.1	FLJ13910	1.7	1.6	2.1	2.5	2.6	2.4	2.5	3.5	1.7	9.0	10.1	8.8	9.8	1.1	2.3	2.4	2.2	1.9	3.8422
209571_at	U03644.1	receptin	0.7	0.2	1.6	3.3	2.7	2.2	1.3	2.6	2.7	6.8	7.8	12.8	10.9	0.8	1.0	1.1	1.2	1.5	3.8367
211317_s_at	AF041461.1	CASP8 and FADD-like apoptosis regulator	1.6	1.8	9.5	3.6	4.0	3.7	6.8	3.2	2.8	33.1	44.8	15.2	17.6	2.4	4.7	6.5	5.7	4.9	3.8332
209732_at	BC005254.1	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2	8.1	5.9	10.0	18.6	23.6	9.0	10.0	8.9	7.3	72.9	77.0	99.7	75.5	4.1	14.4	21.2	10.2	16.4	3.8003
201779_s_at	AF070558.1	clone 24450 RING zinc finger protein RZF	14.8	5.9	13.0	13.3	13.9	21.8	27.0	25.3	13.1	88.2	108.1	116.5	81.8	6.0	9.6	11.3	25.7	15.7	3.7993
212441_at	D86985.2	KIAA0232	5.4	2.9	3.5	9.8	10.3	8.0	6.9	11.5	11.3	31.9	30.1	30.8	49.8	2.5	2.0	4.0	5.9	2.1	3.7868
205920_at	NM_003043.1	solute carrier family 6, member 6 (SLC6A6)	1.2	1.4	0.9	0.2	0.2	1.1	5.2	0.7	1.4	33.1	26.7	2.7	4.0	0.3	0.1	0.4	2.6	0.1	3.7836
213596_at	AL050391.1	DKFZp586A181	0.7	0.7	2.3	3.6	3.0	1.2	1.2	1.1	1.2	10.6	10.9	12.5	9.9	2.2	1.1	2.0	1.5	0.7	3.7615
209508_x_at	AF005774.1	caspase-like apoptosis regulatory protein (clarp)	1.7	2.7	10.8	7.6	11.5	4.9	6.3	6.0	8.4	37.0	34.8	34.7	40.8	2.7	4.0	5.1	6.3	3.4	3.7451
218115_at	NM_018154.1	FLJ10604	0.9	2.2	2.4	1.5	0.9	1.8	2.1	1.3	1.1	10.5	9.1	6.7	7.7	1.1	1.2	2.2	2.1	1.7	3.7435
215652_at	AK024382.1	FLJ14320	0.2	0.1	2.0	0.3	1.6	0.3	0.3	1.2	0.7	5.5	4.5	3.4	2.5	0.1	0.3	1.0	0.9	0.2	3.7249
212561_at	AA349595	RAB6 interacting protein 1	10.0	6.1	10.2	12.4	11.4	18.7	14.9	12.1	10.0	66.3	60.0	47.6	37.1	4.0	8.7	9.9	13.9	5.9	3.6962
204166_at	NM_014963.1	KIAA0963	3.6	0.4	1.1	0.0	0.1	1.0	1.3	0.1	0.8	11.8	12.5	4.0	2.9	0.3	0.9	1.7	1.7	1.2	3.6908
221874_at	AB037745.1	KIAA1324	0.3	0.3	0.7	1.1	0.3	0.8	0.8	0.7	0.5	9.1	5.1	5.1	1.2	0.9	1.1	0.7	0.5	0.6	3.6808
217207_s_at	AK025267.1	butyrophilin like receptor	1.2	1.1	1.4	2.1	1.7	1.2	1.9	0.6	2.4	10.9	3.4	7.2	6.1	1.5	1.7	1.6	0.9	1.5	3.6795
212579_at	AA868754	KIAA0650	1.3	1.6	5.3	9.8	15.5	7.3	7.8	11.3	8.3	32.8	42.9	40.0	39.7	2.0	5.4	5.7	3.1	10.5	3.6784
212657_s_at	AN083357	IL-1 receptor antagonist IL-1Ra (IL-1RN)	48.8	2.3	0.9	0.5	0.6	2.1	0.9	1.5	1.3	35.2	37.0	48.2	35.5	0.6	0.8	0.3	9.3	0.4	3.6759
202392_s_at	NM_014338.1	phosphatidylserine decarboxylase arginase (ARG1)	3.4	2.7	6.2	11.7	6.8	3.4	4.7	5.4	4.7	32.8	31.0	22.0	32.3	0.8	1.6	1.4	4.2	1.4	3.6753
206177_s_at	NM_000045.2	LPS-induced TNF-alpha factor (PIG7)	0.5	1.3	2.2	0.4	0.6	0.9	0.8	7.2	0.7	3.9	4.3	8.1	5.0	1.1	0.1	0.4	0.6	0.7	3.6722
200706_s_at	NM_004862.1	FLJ13910	31.2	39.0	20.7	64.6	62.5	15.6	13.4	31.8	21.7	173.2	148.5	172.0	150.2	8.5	13.3	42.7	14.3	16.7	3.6696
212478_at	AL050139.1	cystatin	0	0.1	0.2	2.3	3.5	1.4	0.8	1.5	1.0	3.7	3.0	4.8	6.5	0.1	0.3	1.1	0.6	0.4	3.6623
218660_at	NM_003494.1	expartin 6	2.5	0.5	1.5	0.2	0.2	1.7	0.2	2.6	1.1	48.5	51.8	44.5	20.4	3.3	1.2	1.7	10.6	0.2	3.6616
211982_x_at	AL546600	guanylate binding protein 2, interferon-inducible (GBP2)	9.8	6.7	14.9	31.8	27.8	24.6	24.0	34.0	24.0	107.2	101.1	86.6	90.2	6.6	17.5	17.4	9.6	11.5	3.6408
202748_at	NM_004120.2	C5a receptor	2.4	5.3	3.7	9.0	7.4	3.3	2.1	3.0	3.3	28.1	35.2	45.0	24.8	4.2	7.3	9.0	6.3	1.9	3.6111
220988_at	NM_001736.1	microtubule-associated protein 7	2.2	2.3	15.4	24.6	24.8	17.1	15.6	9.8	12.0	90.5	104.5	84.4	91.1	2.3	1.2	0.5	25.6	1.0	3.6036
202890_at	T62571	DKFZP434J037	0.9	0.1	0.7	1.4	1.1	0.1	0.0	0.2	0.1	2.5	3.1	3.2	7.1	0.0	0.1	0.4	0.1	0.1	3.6032
220987_s_at	NM_030952.1		1.4	0.3	3.9	4.9	4.7	9.6	9.3	14.1	11.7	43.0	35.6	57.8	57.6	5.3	4.7	4.8	11.1	13.3	3.5748

Fig. 6H

C. Neutrophil (Ne)-selective transcripts (6/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	NeS1
207072_at	NM_003853.1	interleukin 18 receptor accessory protein (IL18RAP)	5.9	0.9	2.2	3.4	4.1	7.2	1.6	2.8	1.7	13.4	9.7	20.9	5.6	2.4	2.8	3.1	0.4	1.6	0.3	3.5722
215719_x_at	X83493.1	CD95, Fas, APO-1	1.0	0.6	3.1	2.7	1.6	2.2	5.2	1.8	1.7	19.0	31.9	11.4	9.4	1.0	4.5	2.2	1.6	1.1	4.4	3.5657
218404_at	NM_013322.1	sorting nexin 10	4.9	1.2	2.6	5.0	3.7	0.7	0.1	2.1	0.7	28.5	31.8	34.8	33.8	0.3	1.2	1.9	9.0	6.5	0.3	3.563
219394_at	NM_024419.1	phosphatidylglycerophosphate synthase (PGS1)	3.4	3.0	1.7	4.2	3.5	2.4	3.8	6.1	9.2	17.2	16.9	17.5	16.3	1.0	2.1	2.6	2.4	1.5	1.7	3.5544
216913_s_at	AK021460.1	KIAA0690	0.1	0.3	0.1	0.1	0.1	1.9	2.5	2.3	2.8	8.9	8.3	7.5	10.9	0.1	0.1	0.2	2.5	0.1	0.0	3.5402
205118_at	M60676.1	formylpeptide receptor 1	0.1	0.2	0.8	0.1	1.1	0.1	0.4	0.6	0.1	3.9	7.0	3.2	7.8	0.2	0.1	0.1	1.4	0.1	0.0	3.5295
210564_x_at	AF009619.1	FLAME-1-delta	1.4	1.5	5.3	6.6	7.0	4.3	4.2	5.9	3.5	21.2	30.3	18.4	19.6	2.1	2.9	4.0	4.6	3.0	1.8	3.5148
213607_x_at	BE551347	KIAA0134	1.3	1.3	2.9	2.0	1.7	8.7	15.8	3.5	4.3	42.7	42.5	11.1	15.3	0.6	1.3	1.9	6.2	1.7	0.9	3.514
203888_at	NM_000361.1	thrombomodulin	0.9	0.6	0.1	0.1	0.3	0.2	0.4	0.8	0.1	6.1	6.4	4.6	0.2	0.3	0.3	0.1	0.6	0.5	0.1	3.5126
210233_at	AF167343.1	interleukin-1 receptor accessory protein (IL1RAP)	0.5	0.1	0.0	0.1	0.6	0.8	0.4	0.6	0.7	1.8	3.0	2.0	2.3	0.6	0.0	0.0	0.0	0.0	0.3	3.5023
204959_at	NM_002432.1	myeloid cell nuclear differentiation antigen	1.2	0.6	24.2	50.0	26.2	17.5	17.9	49.8	22.3	249.8	290.2	186.0	217.0	3.4	1.6	0.6	66.6	2.5	0.0	3.4903
217967_s_at	AF288391.1	niban	6.3	3.7	16.3	42.4	35.9	27.9	29.5	43.0	30.9	107.4	115.3	117.9	110.3	2.6	7.5	9.9	4.9	3.4	20.4	3.4847
221763_at	A1694023	thyroid hormone receptor interactor 8 leukocyte immunoglobulin-like receptor, subfamily A (with TM domain) member 2 (LILRA2)	0.8	1.5	1.9	4.6	5.5	5.5	6.9	9.9	9.0	28.3	32.9	34.0	42.7	1.1	3.7	4.1	5.1	9.8	3.0	3.4777
207857_at	NM_006866.1	solute carrier family 12 member 6 (SLC12A6)	0.4	0.5	3.6	8.5	5.3	4.5	4.9	1.6	6.3	33.5	34.3	46.2	50.8	1.8	0.0	0.1	11.6	0.5	0.1	3.4773
220740_s_at	NM_005135.1	pie-8 cell colony-enhancing factor	1.6	1.0	2.5	3.3	3.4	3.5	5.6	3.2	3.2	12.6	19.0	10.7	14.4	4.0	2.9	2.2	2.9	3.5	0.8	3.4722
217739_s_at	NM_005746.1	orosmuroid 1 (ORM1)	7.1	1.7	9.9	46.0	61.0	18.9	13.9	12.9	9.3	112.4	120.5	90.8	93.4	1.2	2.3	1.4	17.6	2.1	3.1	3.4242
205041_s_at	NM_000607.1	exportin 6	0.3	1.0	0.4	0.1	0.1	0.0	0.1	1.0	0.1	2.6	3.6	2.7	0.4	0.1	0.2	0.1	0.5	0.0	0.1	3.4189
214784_x_at	BE966299	bromodomain adjacent to zinc finger domain, 1A	7.4	5.0	10.0	23.7	23.9	13.0	16.7	23.3	20.5	60.3	67.8	57.2	60.8	2.9	8.7	7.8	6.6	5.9	5.4	3.4155
217985_s_at	AA102574	KIAA0993	1.5	1.4	1.8	2.6	3.8	7.4	5.1	7.3	4.7	16.9	19.2	22.1	24.2	2.7	2.5	2.3	3.5	2.4	0.9	3.3999
212598_at	A1806395	FLJ20847	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	5.5	7.3	3.1	3.2	0.2	0.1	0.0	1.0	0.1	1.3	3.3933
219053_s_at	NM_017966.1	PAC clone RP3-515N1	2.6	2.0	1.9	2.3	2.3	2.6	2.1	3.0	2.8	11.3	7.6	22.2	34.1	1.6	0.5	0.9	4.7	1.3	2.9	3.3686
217475_s_at	AC002073	Ca2+-dependent endoplasmic reticulum nucleoside diphosphatase	0.6	0.5	0.6	0.2	0.4	1.3	1.3	0.5	1.2	5.9	9.8	1.6	1.4	0.7	0.3	0.1	0.5	0.7	0.2	3.3448
46323_at	AL120741	KIAA0625	4.4	3.2	4.2	8.3	7.2	5.3	6.7	11.4	7.9	20.0	21.5	33.9	26.3	2.5	2.8	3.6	4.3	3.4	5.0	3.3028
201965_s_at	NM_015046.1	insulin-like growth factor 1 receptor	2.7	3.1	3.3	8.5	8.3	4.9	5.8	7.4	7.5	19.5	18.5	18.7	27.8	2.2	3.9	3.4	4.6	5.6	2.6	3.3019
203628_at	NM_000875.2	LIM domain kinase 2 (LIMK2)	0.5	0.1	3.7	3.0	4.0	6.8	4.9	2.7	5.8	18.8	23.4	6.8	20.6	1.6	0.1	2.8	2.4	2.0	3.5	3.2989
202193_at	NM_005569.2	transcript variant 2a	1.8	1.5	1.9	5.6	5.6	6.4	4.8	11.3	8.9	17.0	20.5	36.5	28.2	0.1	1.3	1.1	0.6	0.5	0.8	3.2887
203042_at	NM_002294.1	lysosomal-associated membrane protein 2 (LAMP2)	2.4	3.1	1.1	1.7	1.3	5.9	6.4	12.4	10.7	21.3	27.0	44.1	35.4	0.8	0.6	0.5	3.2	0.8	9.4	3.282
220326_s_at	NM_018071.1	FLJ10357	5.1	4.5	1.9	1.2	1.9	6.3	8.9	5.2	8.5	25.3	28.1	19.2	21.0	0.9	0.1	0.7	6.4	0.1	4.1	3.2759
212470_at	AB011088.1	sperm associated antigen 9 clone 6 immunoglobulin-like transcript 5	4.0	2.9	3.3	6.3	7.2	4.5	4.0	4.7	4.9	13.2	17.0	18.1	24.0	1.2	2.5	2.2	3.9	3.0	5.4	3.2688
211133_x_at	AF009643.1	DKFZp434C0328	1.9	1.4	0.8	1.5	1.3	3.1	2.7	3.8	2.1	42.1	42.2	27.0	25.1	2.7	0.9	0.5	10.2	0.4	0.2	3.2526
219313_at	NM_017577.1	G protein-coupled receptor GRP77	0.0	0.8	0.2	0.0	0.4	0.2	0.1	0.1	0.0	3.8	3.7	3.1	5.6	0.2	0.1	0.1	0.0	1.2	0.1	3.2404
221149_at	NM_018485.1	5,10-methylenetetrahydrofolate synthetase	0.2	0.1	0.8	0.7	1.2	0.7	0.9	0.9	0.6	3.3	3.2	4.2	2.9	0.0	0.3	0.2	1.0	0.1	0.3	3.2282
203433_at	NM_006441.1	FADD-like apoptosis regulator	1.4	1.8	1.5	2.5	1.6	3.1	4.2	3.5	3.1	15.8	11.4	9.6	9.0	1.6	1.8	1.9	2.9	1.7	1.5	3.2181
214486_x_at	AF041459.1		1.9	2.1	10.7	5.0	6.5	4.2	5.3	4.3	6.0	26.3	16.2	25.3	24.2	2.4	3.7	5.0	5.3	2.3	1.9	3.2114

Fig. 6I

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C. Neutrophil (Ne)-selective transcripts (7/7).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl	CD4	CD8	CD14	CD19	Fb	Ba.SI.
209272_s_at 202334_s_at	BC000296.1 AA877765	oxysterol binding protein-like 2 ubiquitin-conjugating enzyme E2B kinase 4 FLJ10357	1.3 3.3	0.2 3.4	2.7 4.8	8.8 15.5	8.0 12.1	5.4 5.3	5.4 7.2	7.7 14.7	7.3 12.8	17.2 20.9	18.4 25.6	22.3 43.6	23.9 38.1	0.9 4.0	2.3 4.5	3.4 3.9	2.8 2.5	2.0 4.9	1.3 4.6	3.1877 3.1871
203266_s_at 58780_s_at	NM_003010.1 R4249	mitogen-activated protein kinase FLJ10357	3.7 4.5	2.4 5.4	4.9 1.5	8.2 3.9	6.3 3.0	2.5 7.8	4.8 9.6	6.8 12.8	5.0 16.4	14.7 28.0	15.2 27.6	27.4 46.7	26.9 44.1	2.8 1.2	2.4 0.6	2.6 0.1	2.7 6.5	2.3 0.2	2.7 5.7	3.1804 3.1803
210582_s_at	AL117466.1	LM domain kinase 2	3.8	1.9	4.3	5.1	4.8	8.7	10.3	10.8	9.4	33.9	36.5	30.8	23.8	1.3	1.7	1.8	1.9	0.9	1.4	3.1609
214766_s_at	AL080144.1	ELYS transcription factor-like protein TMBS62	1.3	0.2	2.0	3.1	4.2	1.9	1.4	2.1	2.4	9.4	9.5	9.9	11.3	3.2	1.3	0.8	0.5	1.0	1.3	3.1414
202266_at 203278_s_at	NM_016614.1 NM_016621.1	TRAF and TNF receptor-associated protein (AD022) BRAF35/HDAC2 complex (80 kDa) transmembrane	9.8 2.1	6.2 2.8	9.4 2.7	23.7 14.8	20.9 11.0	8.6 5.7	9.9 5.0	16.5 7.4	14.0 4.9	36.1 21.0	56.5 16.6	64.5 31.0	57.5 30.6	4.5 0.7	7.7 3.0	9.4 4.5	5.3 3.1	8.2 2.7	6.3 3.0	3.1402 3.1382
207291_at 213229_at 204204_at 201364_s_at	NM_024081.1 BF590131 NM_001860.1 AF242521.1	gamma-carboxyglutamic acid protein 4 Dicer1, Dcr-1 homolog (Drosophila) solute carrier family 31 ornithine decarboxylase antizyme clone 17.6 immunoglobulin-like transcript	0.1 8.5 1.7 8.3	1.2 4.5 1.7 7.3	1.3 19.5 1.3 4.4	1.4 12.9 0.3 2.2	1.1 15.4 0.8 1.9	0.9 15.9 1.7 11.5	0.2 9.7 0.9 21.9	0.4 19.1 2.3 8.0	0.2 16.0 1.2 7.7	3.8 35.2 22.6 61.9	7.9 39.0 23.8 59.1	4.5 61.4 31.3 21.0	8.5 69.4 36.0 27.7	0.2 6.2 2.0 2.2	0.8 5.9 1.2 5.1	0.1 7.3 1.2 6.3	1.9 15.2 8.9 12.2	1.1 12.2 0.2 6.2	0.4 5.0 0.4 9.6	3.1336 3.1306 3.1262 3.1253
210784_x_at	AF009634.1	v-yes-1 Yamaguchi-sarcoma viral related oncogene homolog (LYN) hypothetical protein MGC26706 major histocompatibility complex, class I, B	1.4	0.1	2.1	1.2	2.4	2.5	2.2	2.8	2.1	52.1	48.8	31.8	36.3	0.8	0.2	0.2	1.3	0.3	0.2	3.1236
202625_at 221895_at 37384_at	AI356412 AW469184 D13640	retinitis pigmentosa GTPase regulator interacting protein 1 (RPGRI1) Toll-like receptor 2 CD95, Fas, APO-1 KIAA0993 FLAME-1 ninturin 1 intercellular adhesion molecule 3 (ICAM3) carbonic anhydrase IV (CA4) metallophosphoesterase v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN) immunoglobulin superfamily, member 6 (IGSF6) protein kinase C and casein kinase substrate in neurons 2 (PACSIN2)	6.9 2.2 2.5	6.9 0.5 3.0	5.0 5.4 3.4	18.2 5.2 3.8	14.9 5.8 3.8	20.7 5.2 6.7	21.7 3.4 6.6	27.7 7.6 7.6	28.6 5.1 6.6	74.7 14.8 25.2	76.3 12.0 17.9	77.5 24.6 21.3	75.7 19.2 29.4	7.5 2.0 2.6	1.7 2.4 2.5	0.9 2.1 2.5	17.1 5.2 7.4	23.6 1.5 1.8	0.5 1.6 2.8	3.1131 3.11 3.0985
206608_s_at 204924_at 204781_s_at 212606_at 211316_x_at 203045_at	NM_020366.1 NM_003264.1 NM_000043.1 AI806395 AF009616.1 NM_004148.1	regulator of G-protein signaling 1 (RGS1) Toll-like receptor 2 CD95, Fas, APO-1 KIAA0993 FLAME-1 ninturin 1 intercellular adhesion molecule 3 (ICAM3) carbonic anhydrase IV (CA4) metallophosphoesterase v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN) immunoglobulin superfamily, member 6 (IGSF6) protein kinase C and casein kinase substrate in neurons 2 (PACSIN2)	1.1 1.8 2.0 2.0 3.1 4.4	1.4 0.1 1.1 2.0 2.9 2.5	1.2 2.1 5.9 0.0 20.1 3.2	0.8 8.2 11.0 0.7 19.4 6.4	1.0 7.6 8.9 0.6 31.9 4.8	1.1 2.8 5.4 0.7 11.6 10.7	1.0 0.4 4.4 0.0 11.9 9.7	0.5 0.8 6.8 0.1 20.6 18.5	1.4 1.4 7.0 0.1 19.1 12.1	6.1 52.9 20.6 18.0 58.8 29.3	3.4 88.0 27.1 14.3 74.1 34.1	5.3 94.4 27.0 25.0 72.8 44.7	4.7 99.8 29.1 26.9 81.0 46.1	1.5 1.6 0.3 0.1 4.1 0.5	0.9 1.3 5.2 0.2 6.8 1.2	0.8 0.1 5.3 0.3 8.7 1.7	1.3 26.3 4.0 6.6 10.3 8.3	0.5 0.9 2.0 0.0 5.5 0.2	0.7 0.4 3.8 3.4 2.6 2.9	3.091 3.0909 3.0827 3.0797 3.0752 3.0746
204949_at 206208_at 213727_x_at	NM_002162.2 NM_000717.2 AI743654	intercellular adhesion molecule 3 (ICAM3) carbonic anhydrase IV (CA4) metallophosphoesterase v-yes-1 Yamaguchi sarcoma viral related oncogene homolog (LYN) immunoglobulin superfamily, member 6 (IGSF6) protein kinase C and casein kinase substrate in neurons 2 (PACSIN2)	3.0 0.2 2.1	3.7 0.6 1.7	5.7 0.1 5.0	46.3 0.1 15.0	34.5 0.1 12.1	38.9 1.1 8.9	51.6 0.7 13.7	94.5 1.0 25.4	93.7 0.8 23.9	161.1 5.6 49.9	168.3 5.2 28.3	239.1 2.8 59.9	241.1 2.4 75.8	4.5 1.2 0.7	13.6 0.1 4.5	21.0 0.1 6.6	17.6 0.1 5.7	19.9 0.1 5.4	1.3 0.1 3.7	3.0617 3.0572 3.0554
202626_s_at	NM_002350.1	zinc finger protein 267	15.5	9.5	12.1	12.7	14.8	32.6	31.6	54.0	41.0	110.1	115.1	122.7	127.2	18.4	2.1	1.5	36.8	33.0	0.6	3.0541
206420_at	NM_005849.1	zinc finger protein 267	1.1	0.3	0.2	0.4	0.7	1.9	1.2	1.1	1.0	17.5	24.2	30.6	33.3	1.4	0.4	0.4	8.4	0.3	0.3	3.0442
201651_s_at	NM_007229.1	zinc finger protein 267	21.4	17.4	4.6	24.8	20.1	13.3	19.5	33.9	35.3	61.3	72.5	76.1	94.4	24.7	4.9	4.4	8.6	6.1	8.0	3.0391
219540_at	AU150728	zinc finger protein 267	2.0	1.0	1.3	3.7	3.6	2.0	1.5	4.4	3.7	6.7	6.9	9.2	9.9	1.0	2.1	1.3	1.0	1.6	0.1	3.0361
201244_s_at	NM_002880.1	v-rat-1 murine leukemia viral oncogene homolog 1 (RAF1) mitogen-activated protein kinase kinase 4	6.0	5.4	12.4	32.8	33.1	14.9	19.0	27.3	25.7	60.4	58.2	89.2	86.2	2.2	6.6	11.3	12.8	7.6	7.3	3.0329
203265_s_at	AA810268	mitogen-activated protein kinase kinase 4	1.4	1.2	2.8	6.4	4.5	1.7	2.6	3.5	3.1	12.8	12.8	10.4	16.8	1.4	1.4	1.3	1.3	2.5	1.5	3.028
203030_s_at 203739_at	AF007555.1 NM_006526.1	IAR receptor-like protein-tyrosine phosphatase zinc finger protein 217	0.0 1.9	0.0 2.6	1.6 3.0	1.2 18.4	0.1 8.4	0.1 7.6	0.1 8.0	0.1 14.7	0.1 14.9	0.8 37.3	3.0 45.1	1.1 24.4	2.8 27.0	0.1 1.2	0.1 4.6	0.0 5.3	0.1 6.1	0.0 5.5	0.0 3.6	3.0269 3.0158
204747_at 206209_s_at	NM_001549.1 NM_000717.2	interferon-induced protein with tetrapeptide repeats 4 (IFIT4) carbonic anhydrase IV (CA4)	2.0 0.7	3.0 1.0	4.9 0.8	6.0 0.6	3.5 0.6	4.3 2.2	12.4 2.1	4.4 1.5	3.0 2.1	24.2 13.8	27.0 7.4	15.4 4.7	12.0 3.5	0.3 2.1	1.8 1.0	1.2 0.5	6.2 0.9	1.4 1.0	2.6 0.5	3.0143 3.0112

Fig. 6J

D. Mast cell (MC)-selective transcripts (1/2).

Probeset	Accession #	Transcripts	MC cord blood	MC														MCSL				
				lung	Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1	Eo 2	Eo 3 (small)	Eo 4 (small)	Ne 1	Ne 2	Ne 3 (small)	Ne 4 (small)	pl	CD 4		CD 8	CD 14	CD 19	Fb
217023_x_at	AF099143	tryptase beta	169.4	118.7	0.7	1.1	0.4	0.1	0.1	0.5	0.1	0.2	0.1	0.6	0.4	0.3	0.1	0.1	0.2	0.1	0.2	202.148
215382_x_at	AF206666.1	tryptase beta	168.1	108.4	1.7	0.7	0.4	0.2	0.2	0.2	0.1	0.1	0.3	0.1	0.1	0.7	0.1	0.1	0.1	0.1	0.5	172.668
204041_at	NM_000898.1	monoamine oxidase B	23.5	46.9	0.2	0.7	0.1	0.1	0.2	0.6	0.3	0.3	0.1	0.2	0.1	0.2	0.2	0.1	0.2	0.1	0.2	136.311
210084_x_at	AF206665.1	tryptase alpha	131.1	92.3	0.7	1.2	1.2	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.6	0.1	0.0	0.1	0.1	0.1	112.376
216474_x_at	AF206667.1	tryptase beta	210.0	120.9	2.4	2.0	1.4	1.2	0.4	0.2	0.1	0.2	1.1	0.1	0.1	1.8	0.8	0.9	0.9	0.1	0.1	84.3375
205683_x_at	NM_003294.2	tryptase beta	195.5	95.3	2.4	2.7	0.3	0.2	0.2	0.6	0.6	0.4	0.1	0.4	1.0	2.0	0.7	0.2	0.3	0.2	0.1	67.2617
207741_x_at	NM_003293.2	tryptase alpha	175.0	99.7	2.2	2.2	1.8	0.5	0.2	0.3	0.2	0.6	0.2	0.3	0.3	2.2	0.7	0.1	0.5	0.3	0.6	59.015
207134_x_at	NM_024164.2	tryptase beta	214.6	112.3	3.1	3.8	1.7	1.2	0.3	0.8	0.6	0.3	0.8	0.4	0.1	0.5	0.2	0.1	1.1	0.4	0.2	57.1834
205653_at	NM_001911.1	cathepsin G	91.2	57.0	2.7	1.1	0.9	0.9	0.4	3.1	0.8	0.3	1.4	1.6	0.6	0.7	0.2	0.4	1.3	0.3	0.2	51.4749
205266_at	NM_002309.2	leukemia inhibitory factor	17.0	9.8	0.2	0.2	0.3	0.3	0.1	0.2	0.2	0.1	0.2	0.4	0.7	0.1	0.2	0.1	0.1	0.1	0.1	44.3659
210324_at	M17263.1	complement protein C8 gamma	2.9	6.9	0.1	0.1	0.0	0.0	0.0	0.1	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.0	0.0	0.0	0.1	33.806
211743_s_at	BC005929.1	major basic protein	74.3	70.7	1.0	4.7	2.7	0.1	0.7	0.8	0.6	0.2	0.3	0.7	0.2	0.1	0.2	0.2	0.3	0.2	0.3	31.5959
211549_s_at	U63296.1	15-hydroxyprostaglandin dehydrogenase	48.3	48.3	2.1	2.5	1.4	1.5	1.3	0.8	0.9	0.1	0.1	0.2	0.1	1.1	0.5	0.8	0.5	0.5	0.0	24.8454
206726_at	NM_014485.1	prostaglandin D2 synthase	119.0	94.0	5.0	7.8	5.7	0.7	0.1	1.0	0.5	0.2	0.2	0.2	0.6	1.3	0.7	0.3	1.2	0.3	0.0	17.432
205011_at	NM_014622.1	loss of heterozygosity, 11, chromosomal region 2, gene A	76.1	70.9	3.0	6.8	4.5	2.3	1.0	1.4	1.9	0.2	1.1	1.2	1.8	2.9	2.2	1.3	1.7	2.0	2.6	16.2511
205428_s_at	NM_001740.2	calbindin 2	16.7	63.4	1.3	0.7	0.9	0.4	1.6	0.7	1.3	1.8	1.6	3.6	1.5	1.7	0.7	1.1	1.3	0.6	0.9	16.1621
219255_at	NM_024554.1	FLJ11413	10.0	9.2	0.1	0.1	0.1	0.2	0.1	0.6	0.6	0.1	0.6	0.1	0.2	0.1	0.6	0.1	0.6	0.0	0.2	15.639
204468_s_at	NM_005424.1	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains	3.6	2.8	0.5	0.3	0.1	0.0	0.1	0.2	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	0.1	0.0	0.0	14.4259
208343_s_at	AF146343.1	CYP7A promoter binding factor	1.5	0.9	0.0	0.0	0.3	0.1	0.0	0.1	0.0	0.1	0.0	0.2	0.4	0.1	0.0	0.0	0.0	0.0	0.0	13.8025
205051_s_at	NM_000222.1	CD117 C-KIT	92.1	85.8	6.2	8.1	7.3	2.3	5.2	6.5	2.7	0.7	2.1	0.8	1.1	0.8	0.2	0.5	0.1	0.1	0.5	12.3815
210102_at	BC001234.1	loss of heterozygosity, 11, chromosomal region 2, gene A	40.9	41.1	2.8	3.7	4.5	0.3	0.4	0.3	0.6	0.7	0.9	0.2	0.6	1.8	0.8	0.7	1.2	0.6	1.3	11.3619
210796_x_at	D86359.1	siatic acid binding lg-like tectin, sigtec6	17.8	26.0	1.5	1.0	1.1	1.2	1.5	1.3	1.4	1.4	2.3	1.7	1.3	2.0	1.4	1.5	1.8	1.0	0.8	10.5398
206519_x_at	D86358.1	siatic acid binding lg-like tectin, sigtec6	3.4	7.9	0.0	0.3	0.4	0.0	0.0	0.0	0.1	0.0	0.1	0.5	0.2	0.5	0.0	0.0	0.0	0.4	0.0	10.13
206480_at	NM_000897.1	leukotriene C4 synthase	8.8	16.0	0.3	0.2	0.6	2.4	1.6	0.5	0.1	0.2	1.1	0.1	0.1	1.3	0.1	0.3	0.1	0.1	0.4	9.27381
206617_s_at	NM_002910.4	renin-binding protein	10.6	6.2	1.2	0.1	0.4	2.8	1.6	0.5	0.1	0.6	2.1	0.1	0.1	0.9	0.2	0.7	0.3	0.4	0.1	9.18529
208089_s_at	NM_030794.1	tudor domain containing 3	6.0	13.4	0.8	0.6	0.2	0.5	0.7	0.5	0.5	0.1	0.6	0.3	0.0	0.7	0.7	1.1	0.8	0.6	1.0	8.16897
205466_s_at	NM_005114.1	heparan sulfate 3-D-sulfotransferase ADAMTS3 a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 3	18.1	7.2	0.1	0.4	0.1	0.7	0.1	0.3	0.2	0.4	0.1	0.8	0.4	0.1	0.0	0.0	0.2	1.4	0.0	8.15381
214913_at	AB002364.1	tissue-plasminogen activator	6.8	4.3	0.5	0.7	0.8	0.5	0.7	0.6	0.4	0.5	0.4	0.7	1.2	0.7	0.6	0.5	0.4	0.5	0.5	7.2214
201860_s_at	NM_000930.1	siatic acid binding tg-like lectin, sigtec6	22.2	29.7	0.2	0.4	0.1	0.1	0.3	0.5	0.5	0.1	0.1	1.3	0.4	1.6	0.1	0.2	0.6	0.1	3.6	7.10135
206520_x_at	NM_001245.1	LR8 protein	19.0	22.7	2.4	1.1	0.8	1.1	1.5	1.3	1.0	2.0	2.0	0.4	1.4	2.9	2.1	2.3	1.9	1.9	1.2	7.10132
220532_s_at	NM_014020.1	FLJ10305	52.4	18.2	0.8	0.8	1.0	6.4	2.9	1.5	1.2	0.4	0.3	1.4	0.6	2.2	0.6	0.2	5.0	0.1	0.0	6.1662
218169_at	NM_018052.1	nuclear receptor subfamily 1, group 1, member 3	6.2	14.6	0.3	0.2	0.4	0.4	0.3	0.3	0.4	0.6	0.5	0.1	0.1	0.5	0.2	1.4	1.6	0.3	1.0	6.04597
221728_x_at	AK025198.1	tudor domain containing 3	5.6	5.5	0.6	0.9	1.0	0.4	3.6	0.9	0.8	0.7	0.6	1.4	0.9	0.9	0.8	0.7	0.7	0.8	0.5	5.70228
214028_x_at	AU156998	lipase	3.2	11.9	0.9	0.0	0.4	0.8	0.3	0.4	0.7	0.6	0.6	0.1	0.1	0.8	1.2	1.1	0.1	0.7	0.9	5.10738
221552_at	BC001698.1	MKP-1 like protein lyrosine phosphatase (MKP-L)	10.6	3.4	0.9	1.8	1.1	0.9	1.1	1.0	0.9	0.2	0.2	0.7	0.1	0.1	0.2	0.7	0.9	0.3	1.1	5.02434
203367_at	NM_007026.1	heparan sulfate 6-O-sulfotransferase	15.0	45.4	1.2	0.9	0.8	0.9	0.9	0.8	0.1	0.2	0.7	0.4	2.0	0.9	1.0	2.7	0.5	1.4	5.2	5.00514
206997_s_at	NM_004807.1		4.2	3.8	0.2	0.1	0.1	0.4	0.4	0.1	0.3	0.3	0.4	0.3	0.7	0.3	0.2	0.6	0.3	0.8	0.2	4.81127

Fig. 6K

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D. Mast cell (MC)-selective transcripts (2/2).

Probe set	Accession #	Transcripts	MC																				
			cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pI	CD4	CD8	CD14	CD19	Fb	MCS.I.	
207480_s_at 45288_at	NM_020149.1 AA209239	TAL homeobox protein Meis2e lipase	14.0 10.9	14.9 3.0	1.9 0.2	3.6 2.1	4.0 0.8	1.7 0.5	1.9 0.5	5.3 1.3	3.8 0.9	0.3 0.1	0.6 0.1	1.0 0.2	0.3 0.1	0.5 0.4	0.8 0.5	0.4 0.5	0.6 1.3	0.4 1.0	0.8 0.9	4.72642 4.52869	
207039_at 201650_at 214533_at	NM_000077.1 NM_002276.1 NM_001836.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) keratin 19 chymase	7.5 6.2 10.1	3.6 12.0 2.7	0.7 0.0 0.4	0.7 0.0 0.2	0.1 0.3 0.8	0.6 0.1 0.1	0.4 0.0 0.1	0.3 0.0 0.8	0.5 0.0 0.1	0.1 0.1 0.1	1.2 0.1 0.1	0.6 0.1 0.2	1.1 0.1 0.2	0.1 0.1 0.2	0.9 0.0 0.7	0.5 0.1 0.5	0.8 0.1 1.0	0.1 0.0 0.4	1.2 2.0 0.3	4.35629 4.35547 4.27984	
218211_s_at 203916_at	NM_024101.1 NM_003635.1	melanophilin N-deacetylaseN-sulfotransferase	24.8 17.9	29.6 26.7	2.7 3.2	2.5 6.5	1.8 6.8	3.0 2.5	2.5 2.7	1.9 3.6	2.2 3.1	4.6 4.2	4.1 3.4	3.3 5.5	4.1 5.2	6.4 0.9	4.0 3.1	3.2 4.9	2.4 3.3	3.4 2.7	2.7 2.4	4.24499 4.20693	
212336_at 200766_at 202218_s_at 204066_s_at	AB002336.1 NM_001909.1 NM_004265.1 NM_014914.1	erythrocyte membrane protein band 4.1-like 1 cathepsin D delta-6 fatty acid desaturase (FADS6) centaurin, gamma 2	3.8 42.6 18.8 5.3	6.4 39.5 24.5 7.9	0.1 2.5 0.4 0.4	0.2 5.3 0.2 0.4	0.1 4.3 1.0 0.7	0.5 4.3 0.3 0.2	0.1 4.8 0.1 0.2	0.2 3.4 0.8 0.6	0.4 2.7 0.5 0.6	0.1 4.0 0.2 0.3	0.1 6.7 0.1 0.5	0.1 3.1 0.1 0.4	0.5 1.9 0.1 0.4	0.1 2.6 1.6 0.8	0.4 1.6 0.1 0.6	0.2 2.5 0.6 1.6	0.4 10.0 0.1 0.6	0.4 1.6 0.6 1.0	1.2 5.9 5.3 1.6	4.12758 4.1037 4.08548 4.06712	
209644_x_at 221679_s_at 211538_s_at 211548_s_at	U38945.1 AF225418.1 U56725.1 J05594.1	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4) lipase heat shock protein 70kD 15-hydroxyprostaglandin dehydrogenase	14.0 2.8 4.4 82.6	6.4 1.9 7.4 60.0	1.0 0.4 0.3 19.4	1.4 0.9 0.6 26.0	0.7 0.1 0.4 16.3	1.2 0.3 0.6 3.2	1.3 0.4 0.3 2.9	1.7 0.4 0.3 1.8	1.5 0.1 0.9 1.7	1.0 0.1 1.4 0.8	1.6 0.5 0.4 0.5	1.5 0.0 1.0 0.9	2.1 0.5 0.8 0.2	2.3 0.1 1.5 4.1	1.8 0.6 0.5 1.2	1.5 0.6 0.5 0.9	0.9 0.6 0.1 0.1	0.3 0.5 0.7 0.6	2.4 0.2 0.2 0.2	3.88459 3.83039 3.80423 3.49258	
210174_at 219412_at	AF228413.1 NM_022337.1	nuclear receptor subfamily 5, group A, member 2 RAB38, member RAS oncogene	2.9 3.9	3.4 4.0	0.5 0.1	0.5 0.4	0.6 0.3	0.8 0.7	1.1 0.1	0.7 0.2	1.2 0.3	1.1 0.2	0.4 0.2	0.1 1.1	0.4 0.7	0.9 1.2	0.7 0.1	0.2 0.8	0.2 0.4	0.6 0.1	0.3 0.5	3.47124 3.32805	
201850_at 205888_s_at	NM_001747.1 A1962693	gelsolin-like capping protein (actin filament) KIAA0555	70.5 5.4	64.5 4.6	9.6 0.7	30.8 1.6	28.8 1.2	8.1 0.8	7.8 0.7	11.5 0.1	9.9 1.0	2.6 1.3	3.6 0.3	3.0 0.2	2.4 0.6	1.6 1.2	1.1 0.3	1.0 1.5	17.0 0.7	5.8 1.2	5.3 0.4	3.29919 3.25197	
221750_at	BG035985	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	5.0	3.8	0.9	1.5	1.1	1.1	1.2	1.3	1.0	1.3	0.5	0.7	1.2	0.7	0.5	1.1	0.7	1.4	1.2	3.1926	
214218_s_at 218788_s_at	AV699347 NM_022743.1	nuclear receptor subfamily 1, group I, member 3 FLJ21080	3.5 16.1	3.5 23.7	0.7 0.5	0.6 2.3	0.7 2.5	0.5 0.9	2.2 1.1	0.5 2.7	0.7 2.1	1.2 1.1	1.2 1.0	0.6 0.8	0.1 0.9	1.1 2.3	0.9 2.1	0.3 2.9	0.6 0.6	0.8 2.0	0.4 6.3	3.15254 3.07851	
218087_s_at 221577_x_at 35820_at 208744_x_at	NM_015385.1 AF003934.1 X62078 BG403660	SH3-domain protein 5 (ponsin) prostate differentiation factor GM2 activator protein heat shock 105kD	1.4 7.8 21.8 7.3	1.9 5.5 17.6 4.8	0.4 0.6 1.4 0.5	0.9 0.3 3.3 0.2	0.4 0.5 1.3 0.2	0.5 0.6 0.3 0.9	0.0 0.1 0.3 0.1	0.0 0.2 0.2 0.4	0.1 0.6 0.5 0.6	0.1 0.0 0.5 0.1	0.1 0.2 0.8 0.1	0.1 0.3 1.9 0.3	0.1 0.7 0.4 0.1	0.0 0.2 0.4 0.8	0.2 0.0 0.2 1.7	0.2 0.1 6.5 2.0	0.2 0.1 0.9 0.9	0.1 2.1 5.0 2.0	3.07366 3.05532 3.01647 3.00671		

Fig. 6L

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E. Basophil and eosinophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pI	CD4	CD8	CD14	CD19	Fb	Ba+Eo.SI
211517_s_at	M96651.1	IL-5R interleukin 5 receptor alpha	0.6	0.1	11.8	28.2	17.9	16.4	25.3	32.6	29.5	0.0	0.7	0.0	1.0	0.0	0.4	0.2	0.0	0.2	0.0	61.956
210744_s_at	M75914.1	IL-5R interleukin 5 receptor alpha	0.2	1.6	15.4	30.8	15.3	18.7	40.2	29.7	33.0	0.3	0.2	1.5	0.5	0.1	0.1	0.1	0.1	0.2	0.1	42.811
206361_at	NM_004778.1	CRTH2 chemoattractant receptor-homologous molecule expressed on Th2 cells	1.8	0.3	22.0	40.5	15.3	33.7	37.9	38.9	42.3	1.0	2.6	2.2	2.1	0.8	1.4	1.0	1.2	0.9	0.5	16.642
206207_at	NM_001828.3	Charcot-Leyden crystal protein	1.1	0.1	270.0	219.1	203.6	226.8	233.8	179.7	163.1	2.1	19.4	19.1	49.3	2.8	1.0	1.4	0.9	0.7	0.4	15.164
203638_s_at	NM_022969.1	fibroblast growth factor R2	0.2	0.1	7.3	43.5	33.0	4.1	8.8	12.3	23.3	0.1	0.1	0.3	0.3	0.1	0.1	0.2	0.1	0.1	1.0	13.357
207111_at	NM_001974.1	egf-like module containing, mucin-like, hormone receptor-like sequence 1 (EMR-1)	1.5	0.1	16.4	49.5	34.5	85.9	93.1	91.2	93.5	2.7	3.7	5.4	5.1	3.4	1.7	0.8	7.1	1.6	0.5	8.0092
215248_at	AU145003	FLJ11581 fs, clone HEMBA 1003598	0.7	0.3	5.7	4.7	5.2	4.5	2.1	2.8	2.1	1.0	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.2	7.2618
205471_s_at	AW772082	dachshund (Drosophila) homolog	0.1	0.6	5.1	4.1	3.7	6.4	8.3	9.0	7.6	0.8	0.9	1.0	0.8	0.1	0.1	0.3	0.5	0.0	0.1	6.8198
218857_s_at	NM_025080.1	FLJ22316	1.0	7.0	18.0	35.3	18.6	13.7	12.5	16.3	15.4	1.3	1.7	0.9	1.9	0.3	0.5	0.4	2.4	0.2	0.2	6.5045
221169_s_at	NM_021624.1	histamine receptor H4	0.2	0.5	4.5	12.5	8.9	1.9	2.6	4.2	2.9	0.5	0.6	1.1	0.6	0.4	0.7	0.5	0.7	0.0	0.3	5.9783
201769_at	NM_014666.1	entropin	7.8	9.1	41.7	101.5	76.0	26.8	34.1	40.5	35.7	3.0	2.9	3.6	4.2	4.5	6.3	6.9	8.0	9.0	7.9	5.1015
208228_s_at	M87771.1	secreted fibroblast growth factor receptor (K-sam_III)	0.3	1.4	3.7	10.2	8.3	3.9	8.9	4.5	8.3	0.8	1.4	1.1	0.5	1.3	0.4	0.7	0.3	0.5	1.1	4.9922
213605_s_at	AL049987.1	hypothetical protein, MNCb-4779	0.8	0.0	10.8	46.8	44.7	6.7	6.1	25.8	20.6	1.3	1.4	4.5	4.2	2.9	1.1	2.1	3.7	2.0	0.3	4.7426
205382_s_at	NM_001928.1	adipsin	3.5	0.1	62.0	206.0	176.5	62.4	48.1	60.5	44.8	7.1	32.5	20.5	16.3	0.1	0.6	0.1	15.6	0.1	3.8	4.7202
49452_at	A057637	hypothetical protein LOC283445	0.6	0.2	5.2	7.7	6.6	6.9	5.9	10.2	12.7	1.1	0.2	0.3	1.3	0.1	1.6	1.6	0.5	1.3	0.8	4.7183
220307_at	NM_016382.1	CD244 natural killer cell receptor 2B4	0.5	0.1	15.7	87.0	65.4	9.9	10.8	26.6	18.5	0.3	0.4	1.2	3.0	0.1	0.4	3.5	5.2	1.1	0.1	4.6297
210108_at	BE550599	calcium channel, voltage-dependent, L-type, alpha 1D subunit	0.2	0.1	1.0	1.7	2.4	0.9	0.8	2.4	1.8	0.0	0.6	0.5	0.5	0.0	0.3	0.1	0.0	0.3	0.0	4.5958
209193_at	M24779.1	protein kinase-related oncogene (Plm1)	6.8	7.1	61.3	110.3	100.1	47.0	79.7	91.6	79.5	19.2	18.8	21.1	16.1	4.1	12.7	13.9	4.6	4.0	1.2	4.1983
202794_at	NM_002194.2	inositol polyphosphate-1-phosphatase (INPP1)	5.7	6.2	7.1	25.8	20.5	17.9	24.8	53.6	57.8	2.8	2.7	2.6	4.0	1.9	1.8	2.6	4.8	1.9	4.8	4.1158
208304_at	NM_001837.1	CCR3 chemokine (C-C motif) receptor 3	0.2	1.1	107.2	142.9	102.2	46.4	91.7	118.1	107.5	28.3	20.0	26.3	25.1	0.2	0.5	0.4	0.2	0.2	0.4	3.9525
206111_at	NM_002934.1	eosinophil-derived neurotoxin	2.2	2.0	33.7	71.4	38.4	104.7	80.8	47.7	45.1	2.0	2.3	3.1	2.8	1.4	0.7	0.4	14.8	0.7	0.5	3.7641
43427_at	A1970898	hypothetical protein LOC283445	0.8	0.7	2.1	4.8	4.3	5.1	4.6	8.0	6.4	1.0	0.8	0.7	0.8	1.1	1.0	1.3	0.6	1.1	1.1	3.7554
213804_at	A039084	inositol polyphosphate-5-phosphatase, 75kD	0.6	1.2	4.3	8.0	6.8	8.6	5.6	6.3	9.7	0.7	0.5	2.2	1.7	1.4	1.2	1.4	1.0	1.9	1.3	3.6088
209906_at	U62027.1	Ga receptor	12.4	11.2	44.1	72.3	50.5	18.8	38.8	70.3	29.9	1.2	1.2	1.8	3.8	1.6	1.6	1.5	3.0	0.6	0.5	3.6039
202804_at	A1539710	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	8.5	7.0	24.2	56.2	48.9	14.2	20.0	30.1	20.7	3.0	3.6	4.3	6.0	3.8	3.5	5.4	5.1	5.5	5.3	3.5673
221675_s_at	AF195624.1	cholinephosphotransferase 1 beta	7.0	6.8	31.6	79.7	55.8	26.9	32.6	43.8	41.8	5.2	7.5	5.9	9.6	2.4	3.1	3.3	7.7	11.8	5.7	3.5626
201562_s_at	NM_003104.1	sorbitol dehydrogenase 1 (SORD)	2.0	1.5	2.9	4.2	4.1	7.4	11.6	8.3	11.2	1.7	2.5	1.5	1.3	1.3	1.4	1.8	1.2	1.8	1.1	3.5098
210230_at	BC003629.1	FLJ23438 fs, clone HRC13275	1.1	0.1	8.3	11.0	13.3	2.4	5.1	5.1	4.1	0.1	0.5	0.2	0.7	0.3	0.2	0.6	0.8	1.9	0.5	3.2532
219919_s_at	NM_018276.1	FLJ10928	0.1	0.2	3.1	1.8	2.5	1.7	4.3	1.7	2.1	0.1	0.5	0.4	0.3	0.1	0.1	0.1	0.1	0.1	0.7	3.2497
204301_at	NM_014867.1	KIAA0711	0.6	0.1	3.8	14.3	10.7	5.3	6.8	12.6	10.5	1.2	0.6	1.6	1.6	1.0	0.8	1.2	2.6	0.8	0.1	3.2398
210999_s_at	U66065.1	Glo 10- and Grib-IR-related splice variant 1	3.6	1.7	8.4	13.6	11.8	7.3	4.6	4.8	6.4	2.2	1.7	1.9	2.0	1.9	1.2	1.2	1.6	0.4	1.6	3.1044
209539_at	D25304.1	RacCdc42 guanine exchange factor (GEF) 6	13.1	24.8	28.8	74.7	73.0	53.8	35.5	92.9	59.6	9.2	6.1	18.5	13.7	3.1	10.8	12.9	7.1	7.8	1.0	3.0943
208921_s_at	L12387.1	sorcin (SRI) bifunctional ATP	19.2	11.4	20.2	88.6	67.0	37.4	42.4	86.3	85.4	6.9	8.9	17.6	21.5	2.6	11.1	12.7	8.4	8.6	17.8	3.0628
209043_at	AF033026.1	sulfurylaseadenosine 5-phosphosulfate kinase	19.9	16.1	39.0	87.1	75.2	66.4	68.7	89.4	71.4	13.8	20.0	46.5	8.9	6.3	6.7	4.4	10.6	11.0	22.7	3.0385

Fig. 6M

E. Eosinophil and neutrophil-selective transcripts (1/1).																						
Probe set	Accession #	Transcripts	MC.																			
			cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	Eo 1	Eo 2	Eo3 (small)	Eo4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pI	CD4	CD8	CD14	CD19	Fb	Eo+Ne S.I.
221345_at	NM_005306.1	GPR43 PARI-like zinc finger, DHHC domain containing 18	0.1	0.4	0.9	0.6	0.6	7.0	16.6	15.4	10.5	49.7	45.7	22.5	23.0	0.8	0.1	0.1	0.7	0.4	0.1	21.742
212860_at	BG168720	solute carrier family 19 member 1	2.2	0.8	4.1	3.9	4.0	16.0	17.4	14.8	16.7	59.2	53.9	30.9	39.8	1.1	2.4	3.8	2.6	1.5	1.3	6.5842
211576_s_at	BC003068.1	nephroblastoma overexpressed gene	1.4	0.1	0.7	1.4	0.7	5.1	5.9	11.5	12.4	19.8	18.7	27.1	28.1	1.8	0.9	0.4	2.7	0.5	0.8	4.99
214321_at	BF440025	ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3	1.3	1.0	0.8	0.2	0.7	6.2	7.2	17.0	13.7	4.5	7.6	10.7	11.3	0.1	0.1	0.0	0.1	0.1	1.8	4.9823
218950_at	NM_022481.1	BCL2-related protein A1	1.4	3.1	2.4	3.7	2.1	15.5	15.9	18.3	15.5	28.0	24.3	15.9	20.6	0.7	0.2	0.8	3.9	0.9	1.0	4.829
205681_at	NM_004049.1	grancalcin	0.5	1.9	1.0	3.2	2.4	52.4	40.2	35.9	30.5	46.5	49.2	35.5	33.5	1.5	2.2	1.9	8.3	4.3	0.2	4.7782
203765_at	NM_012198.1	CDNA FLJ36416 f1s, clone	2.0	1.8	4.5	11.7	8.3	27.5	39.8	46.7	34.8	71.6	85.2	80.5	77.9	1.0	1.0	1.2	12.1	3.1	0.5	4.4403
213241_at	AF035307.1	THYMU2011053	5.0	2.4	1.6	1.0	1.0	33.2	37.1	68.7	40.6	63.2	77.8	89.2	80.9	3.0	3.0	2.8	13.5	4.1	7.8	4.2603
221815_at	BE671816	hypothetical protein PRO2831	1.2	1.4	1.3	0.5	1.6	10.1	8.8	11.2	6.4	5.0	6.2	4.0	3.8	1.6	0.8	0.2	1.4	0.9	0.6	4.1325
214153_at	BE467941	homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	1.0	0.6	1.0	2.0	3.1	9.1	10.4	18.2	16.6	9.7	9.7	14.5	15.2	0.8	0.9	1.2	0.7	2.3	0.1	4.0797
212821_at	AU147160	KIAA0599	0.1	0.1	0.4	1.2	0.9	4.6	2.8	4.7	3.4	4.4	3.5	6.0	7.9	0.4	0.2	0.4	0.3	0.0	0.2	3.727
206723_s_at	AF011466.1	Edg4, endothelial differentiation lysophosphatidic acid	1.2	1.4	2.1	3.6	2.6	13.7	8.0	19.6	22.3	24.6	17.0	26.1	29.1	0.1	3.6	5.0	3.8	1.9	0.9	3.7119
212360_at	A1916249	G-protein-coupled receptor, 4 adenosine monophosphate deaminase 2 (isoform L)	1.0	2.0	2.6	5.9	4.6	26.6	18.7	30.2	31.9	78.7	63.1	79.5	91.3	3.4	5.8	6.1	12.6	3.7	5.8	3.5888
218308_at	NM_006342.1	transforming, acidic coiled-coil containing protein 3 (TACC3)	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769
212629_s_at	AK023692.1	protein kinase C-like 2	1.9	0.6	3.1	3.7	5.1	11.8	7.6	17.7	13.8	16.7	23.6	27.0	28.4	1.1	2.1	2.2	4.2	4.2	2.9	3.2963
201739_at	NM_005627.1	serumglucocorticoid regulated kinase (SGK)	30.2	25.2	1.9	18.5	25.4	114.1	116.0	150.9	164.8	60.2	77.1	105.8	156.3	1.1	3.7	0.7	34.6	1.6	18.9	3.2456
209473_at	AV717590	ectonucleoside triphosphate diphosphohydrolase 1	1.4	0.6	2.1	1.6	2.0	15.9	22.3	39.5	29.1	14.1	13.7	23.7	13.8	2.6	2.6	1.3	6.5	4.8	0.6	3.0752
209304_x_at	AF087853.1	growth arrest and DNA damage inducible protein beta (GADD45B)	2.0	0.3	2.7	4.5	3.6	15.5	11.9	16.3	34.4	7.0	12.0	13.5	9.4	0.4	3.1	4.2	4.1	3.7	0.6	3.0295
210666_at	AF050145.1	iduronate 2-sulfatase	0.1	0.3	1.3	0.5	1.7	7.1	2.9	3.3	3.8	6.1	5.1	5.2	10.8	0.4	0.1	0.9	0.7	0.4	0.1	3.0005

Fig. 6N

G. Basophil and neutrophil-selective transcripts (1/1).

Probe set	Accession #	Transcripts	MC																			
			cord blood	MC lung	Ba1 (small)	Ba2 (small)	Ba3 (small)	EO 1	EO 2	EO 3 (small)	EO4 (small)	Ne 1	Ne 2	Ne3 (small)	Ne4 (small)	pl CD4	CD8	CD14	CD19	Fb	Ba+Ne S.L.	
218739_at	NM_016006.1	CGI-58 protein	1.8	1.8	7.2	16.3	17.3	2.6	3.3	3.2	2.5	20.7	23.6	21.4	19.3	1.3	1.2	0.7	2.9	0.7	1.5	5.81398
219242_at	NM_025180.1	FLJ13386	1.0	0.3	10.1	23.5	18.8	2.4	3.7	4.5	4.2	13.7	14.0	26.1	27.7	0.1	0.5	1.6	1.0	0.6	2.5	4.97025
219157_at	NM_007246.1	kelch (Drosophila)-like2	2.4	1.7	4.2	16.2	19.2	3.6	2.5	4.3	3.8	15.5	24.4	24.5	22.5	0.7	2.0	1.5	3.0	2.2	1.7	4.61523
206643_at	NM_002108.2	histidine ammonia-lyase	0.1	1.4	8.5	13.7	25.4	0.2	0.6	1.3	0.6	31.4	32.8	61.7	37.0	1.6	0.5	0.1	5.6	0.6	0.5	4.57355
213935_at	AF007132.1	clone 23551 mRNA	0.8	0.1	5.0	26.2	26.4	2.4	1.7	2.9	1.2	4.5	6.7	11.2	9.0	0.1	0.1	0.2	2.3	0.5	0.8	4.33664
222151_s_at	AK023738.1	FLJ13676 fis	1.0	0.9	4.5	5.5	4.7	1.8	1.7	1.4	1.6	8.4	10.2	8.4	7.6	0.5	0.8	1.3	0.8	1.0	1.3	4.14372
207907_at	NM_003807.1	tumor necrosis factor (ligand)	0.1	0.1	3.9	10.4	6.3	1.2	1.5	4.0	4.1	15.8	7.3	15.8	11.5	0.2	0.4	0.1	0.6	0.0	0.1	3.89177
202530_at	NM_001315.1	superfamily member 14 (TNFSF 14)	5.0	3.0	28.8	82.2	70.8	4.0	7.1	13.9	11.1	13.6	23.0	25.7	22.3	5.3	2.9	3.5	7.3	2.6	4.5	3.8469
217521_at	N54942	mitogen-activated protein kinase 14	0.1	0.1	5.5	18.9	20.9	0.3	0.3	1.6	0.1	19.6	14.5	29.9	18.4	0.4	0.8	0.9	4.3	1.0	0.3	3.84207
203693_s_at	NM_001949.2	Hs276590 ESTs	2.5	1.7	4.3	16.2	13.2	2.1	1.9	5.7	3.3	8.8	11.7	13.3	15.4	1.5	1.4	2.5	2.3	1.1	1.2	3.7116
203420_at	NM_016255.1	E2F transcription factor 3	2.4	3.3	15.6	31.5	32.4	7.3	6.6	14.3	11.0	37.2	37.2	48.5	50.0	6.1	5.0	9.8	4.5	3.3	9.8	3.48188
218308_at	NM_006342.1	autosomal highly conserved protein (AHCP)	0.4	0.4	4.8	8.3	9.5	3.3	2.4	3.3	4.7	17.6	14.8	23.5	22.8	2.4	2.3	1.6	3.6	1.0	0.7	3.4769
203080_s_at	NM_013450.1	transforming acidic coiled-coil	2.2	2.4	10.4	22.8	22.9	4.9	6.6	10.0	9.5	29.5	30.7	33.5	40.6	1.1	1.7	1.9	4.6	2.3	1.5	3.401
219999_at	NM_018621.1	containing protein 3	0.4	0.6	3.9	7.6	8.0	2.0	1.5	3.9	2.7	9.8	6.5	11.7	12.3	0.2	1.3	1.8	2.4	1.7	0.9	3.31991
213805_at	AI692428	bromodomain adjacent to zinc finger domain, 2B	0.3	0.1	13.8	11.0	8.7	3.2	3.0	1.4	1.4	19.7	16.7	5.3	7.0	0.7	0.2	0.8	3.3	0.4	0.7	3.29317
204669_s_at	NM_007219.2	hypothetical protein PRO2198	0.9	0.2	4.4	27.9	34.3	2.1	5.9	16.1	14.5	18.8	14.4	60.7	56.1	0.5	0.1	0.1	0.1	0.1	0.8	3.18834
215555_at	AK023774.1	clone 23551 mRNA	0.0	0.4	5.0	4.3	5.8	1.5	1.9	1.5	1.5	7.6	8.2	3.3	3.2	0.9	1.0	1.5	1.5	1.0	0.1	3.1591
		ring finger protein 24																				
		FLJ13712 fis																				

33/36

Fig. 60

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H. Mast cell and basophil-selective transcripts (1/1).		MC													
Probe set	Accession #	Transcripts	MC	Ba1	Ba2	Ba3	Eo	Eo	Eo3	Eo4	Ne	Ne	Ne3	Ne4	
205624_at	NM_001870.1	carboxypeptidase A3	cord blood	91.0	139.0	173.1	2.5	1.6	2.8	1.9	0.1	1.4	2.0	12.4	59.1989
208605_s_at	NM_002529.2	R	lung	1.2	9.3	8.1	0.2	0.2	0.0	0.1	0.2	0.0	0.1	0.1	34.7309
210258_at	AF030107.1	TRK neurotrophin receptor		8.4	7.1	10.9	0.3	0.1	0.4	0.5	0.5	0.0	0.1	0.3	
207496_at	NM_000139.1	regulator of G protein signaling (RGS13)		24.7	51.9	45.6	0.9	0.1	0.5	0.3	0.1	0.1	0.5	1.8	21.7762
205857_at	A1269290	R		27.1	22.3	25.0	1.3	1.0	0.8	0.9	1.3	0.9	0.5	0.7	21.1783
210358_x_at	BC002557.1	GATA-binding protein 2		18.4	31.7	24.7	2.0	1.6	1.9	1.7	0.9	1.9	1.3	3.7	20.3301
207497_s_at	D10583.1	Fc epsilon R1 beta		10.7	12.6	6.8	1.5	1.0	0.8	0.8	1.9	0.9	1.7	1.5	94.6893
203914_x_at	NM_000860.1	15-hydroxyprostaglandin dehydrogenase (PDGH)		63.9	36.0	23.3	4.1	4.6	4.6	0.8	1.9	0.9	1.7	1.5	93.9967
219557_s_at	NM_020645.1	chromosome 11 open reading frame 14		51.4	24.8	23.3	4.1	4.6	4.6	2.6	1.3	0.9	1.3	1.2	6.14285
204061_at	NM_005044.1	protein kinase, X-linked		7.4	7.4	6.6	1.2	1.6	2.0	2.4	0.9	1.9	1.1	2.1	3.38029
202068_s_at	NM_000527.2	R		6.2	12.8	16.9	2.3	2.7	2.5	2.4	0.8	0.4	0.7	1.2	3.26062
		low density lipoprotein receptor		24.6	19.3	13.5	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	3.1679
				16.8	28.5	13.5	1.6	1.0	1.6	0.9	0.8	2.4	1.5	2.5	

Fig. 6P

I. Specific transcripts markers for non-granulocytes.																								
ProbeSet	Accession #	Transcripts	MC		Ba 1	Ba 2	Ba 3	Eo 1	Eo 2	Eo 3	Eo 4	Ne 1	Ne 2	Ne 3	Ne 4	pl	CD 4	CD 8	CD 14	CD 19	Fb			
			cord	lung																				
203547_at	U47924	CD4	5.5	4.7	2.2	1.1	1.2	2.0	1.6	0.4	0.9	0.7	1.1	0.7	0.8	3.5	150	0.3	17.6	1.2	0.4			
205758_at	AW006735	CD8	0.5	1.7	2.6	2.3	3.2	1.3	1.1	2.2	1.7	0.3	0.5	1.8	0.3	4.2	3.0	76.1	0.8	0.6	0.4			
206398_s_at	NM_001770.1	CD19	0.7	0.1	0.7	0.4	0.7	0.8	0.5	0.5	0.2	0.6	1.5	1.1	0.7	4.0	0.0	0.1	0.1	19.1	0.4			
211644_x_at	L14458.1	IgGV-J region	0.2	0.1	0.1	0.1	0.2	0.2	0.2	0.2	0.3	0.1	0.3	0.2	0.2	3.8	0.1	0.2	0.1	70.9	0.1			
201743_at	NM_000591.1	CD14	18.4	2.4	0.3	0.1	0.6	8.8	0.6	1.1	3.2	40.7	49.6	58.7	68.2	2.9	0.4	0.0	97.2	1.1	0.9			
203104_at	NM_005211.1	v-fms M-CSF receptor	3.8	0.2	0.6	0.7	0.3	3.0	1.1	1.7	1.5	8.8	8.7	6.3	6.4	5.2	2.8	0.7	42.1	1.4	0.9			
209968_s_at	U63041.1	CD56	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.2	0.1	0.1	0.1	0.1	0.2	0.1	0.0			
204627_s_at	M35999.1	CD61 glycoprotein IIIa	1.7	9.4	0.2	0.1	0.3	0.1	0.1	0.1	0.1	0.1	0.4	0.1	0.2	48.3	0.1	0.3	0.1	0.2	0.5			
216442_x_at	AK026737.1	fibronectin	0.3	1.5	0.3	0.3	0.2	0.1	1.0	0.3	0.6	0.1	0.1	0.2	0.1	0.3	0.1	1.0	0.3	0.1	92.6			

Fig. 6Q

J. Raw AD levels for the median values used to normalize the raw AD levels, and the housekeeping genes.

Probe set	Accession #	Transcripts	MC		Ba 1 (small)	Ba 2 (small)	Ba 3 (small)	Eo 1 (small)	Eo 2 (small)	Eo 3 (small)	Eo 4 (small)	Ne 1 (small)	Ne 2 (small)	Ne 3 (small)	Ne 4 (small)	pl	CD 4	CD 8	CD 14	CD 19	Fb
			cord	lung																	
AFFX-HSAC07/X00351_3_at	X00351	beta-actin	18534	19383	14638	20922	19151	22019	18638	21153	18568	19406	22302	16589	17569	18295	18782	20805	20661	17542	20399
AFFX-HSAC07/X00351_M_at	X00351	beta-actin	22898	21777	12940	11533	7608	22560	18785	14861	13431	23106	23373	6861	8019	19368	20362	22761	22294	19087	22757
AFFX-HSAC07/X00351_5_at	X00351	beta-actin	15642	15838	9516	2927	2066	17186	21061	4861	3771	18772	19768	2165	2193	14887	16381	18218	17583	15063	16795
AFFX-HUMGAPDH/M33197_3_at	M33197	GAPDH	14906	13632	3640	10477	9332	2649	2844	5498	2605	2549	3186	3586	3538	5929	6429	6098	9756	5180	19674
AFFX-HUMGAPDH/M33197_M_at	M33197	GAPDH	15891	16852	3218	7587	6963	2382	2565	3720	1838	2194	2796	2312	2154	6182	5931	5921	11464	4344	17013
AFFX-HUMGAPDH/M33197_5_at	M33197	GAPDH	16298	16701	3479	4559	5110	1827	3121	2127	1168	2492	3476	1636	1355	4655	6826	6260	9905	5636	23350
The median value of 2283 transcripts			121	1693	853	1122	1109	93.7	102.1	127.3	114	62.7	73.1	87.4	87.3	82.3	152.5	121.3	107.1	114.1	183.8

Abbreviations used in the table A-I were (small); the results obtained by the small sample protocol (see materials and methods), R; receptor, and ICN; ion channel.

Fig. 6R